179743 *M?*

From: Chan, Christina
Sent: Wednesday, February 15, 2006 5:48 PM
To: Steadman, David (AU1652); STIC-Biotech/ChemLib
Subject: RE: RUSH sequence search request for 10/049,429

Please rush. Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

RECEIVED (STIC) FEB 16 2006

-----Original Message-----
From: Steadman, David (AU1652)
Sent: Wednesday, February 15, 2006 3:39 PM
To: Chan, Christina
Subject: RUSH sequence search request for 10/049,429

Ms. Chan,

An after-final amendment has been filed in 10/049,429 and the claim appears to be in condition
for allowance. I would like to request a RUSH sequence search. Both SEQ ID NO:1 and 17 are
recited in the claim. SEQ ID NO:1 is 211 amino acids and SEQ ID NO:17 is 132 amino acids.
Thank you -

David

NAME: David Steadman
AU: 1656
Date: 2/15/06
Office: Remsen 2B05
Mailbox: Remsen 3C70

Please perform the following searches in commercial and interference databases:

1) Standard search of SEQ ID NO:1 against amino acid databases.

2) Standard search of SEQ ID NO:1 against nucleic acid databases.

3) Standard search of SEQ ID NO:17 against amino acid databases.

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4) Standard search of SEQ ID NO:17 against nucleic acid databases.

Please save results to diskette.

Thank you very much.

David J. Steadman, Ph.D.
Primary Examiner
Art Unit 1656
Protein Crystallography and Recombinant Enzymes
Office: Remsen 2B05
Mailbox: Remsen 3C70
Phone: (571) 272-0942

****
Searcher:_____
Searcher Phone:_____
Date Searcher Picked up:_____
Date completed:_____
Searcher Prep Time:_____
Online Time:_____

****
Type of Search
NA#_____ AA#:_____
S/L:_____ Oligomer:_____
Encode/Transl:_____
Structure #:_____Text:____
Inventor:_____ Litigation:___

****
Vendors and cost where applicable
STN:_____
DIALOG:_____
QUESTEL/ORBIT:_____
LEXIS/NEXIS:_____
SEQUENCE SYSTEM:_____
WWW/Internet:_____
Other (Specify):_____

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OM protein - protein search, using sw model

Run on: February 18, 2006, 14:52:11 ; Search time 186 Seconds
                                         (without alignments)
                                         498.435 Million cell updates/sec

Title: US-10-049-429-1
Perfect score: 1144
Sequence: 1 MPVAPYWTSPEKMEKKLHAV.........TCLAGNSIGLSHHSAWLTVL 211

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_21:*
                1: geneseqp1980s:*
                2: geneseqp1990s:*
                3: geneseqp2000s:*
                4: geneseqp2001s:*
                5: geneseqp2002s:*
                6: geneseqp2003as:*
                7: geneseqp2003bs:*
                8: geneseqp2004s:*
                9: geneseqp2005s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1144	100.0	284	9	AEB55445	Aeb55445 FGFR1 pro
2	1144	100.0	287	3	AAB36230	Aab36230 Human FGF
3	1144	100.0	373	9	AEB55448	Aeb55448 FGFR1 pro
4	1144	100.0	432	9	ADZ12925	Adz12925 Human can
5	1144	100.0	609	7	ABM85323	Abm85323 Human pro
6	1144	100.0	660	9	ADZ12923	Adz12923 Human can
7	1144	100.0	662	9	ADX69340	Adx69340 Human hep
8	1144	100.0	702	5	ABG79680	Abg79680 Tumour in
9	1144	100.0	733	9	ADW12713	Adw12713 Human fib

10	1144	100.0	759	9	ADY57312	Ady57312	Human fib
11	1144	100.0	783	9	ADZ12915	Adz12915	Human can
12	1144	100.0	820	8	ADS18132	Ads18132	Human FGF
13	1144	100.0	820	9	ADZ12913	Adz12913	Human can
14	1144	100.0	822	2	AAR13549	Aar13549	Basic FGF
15	1144	100.0	822	2	AAR20750	Aar20750	flg recep
16	1144	100.0	822	2	AAR26337	Aar26337	N-sam. 2/
17	1144	100.0	822	6	AAE34488	Aae34488	Human FGF
18	1144	100.0	822	7	ABR56164	Abr56164	Human Fib
19	1144	100.0	822	7	ADE61700	Ade61700	Human Pro
20	1144	100.0	822	7	ADF45057	Adf45057	Human kin
21	1144	100.0	822	7	ADP65260	Adp65260	Human fib
22	1144	100.0	822	7	ADP65261	Adp65261	Human fib
23	1144	100.0	822	8	ADO42159	Ado42159	Human NOV
24	1144	100.0	822	8	ADQ17658	Adq17658	Human sof
25	1144	100.0	822	8	ADP24447	Adp24447	PRO polyp
26	1144	100.0	822	9	ADW12711	Adw12711	Human fib
27	1144	100.0	822	9	ADY16516	Ady16516	PRO polyp
28	1140	99.7	373	9	AEB55447	Aeb55447	FGFR1 pro
29	1139	99.6	282	9	AEB55446	Aeb55446	FGFR1 pro
30	1139	99.6	351	2	AAY21643	Aay21643	FGFR 1 (f
31	1139	99.6	371	9	AEB55444	Aeb55444	FGFR1 pro
32	1139	99.6	432	9	ADZ12906	Adz12906	Murine ca
33	1139	99.6	451	7	ABM85322	Abm85322	Mouse pro
34	1139	99.6	488	3	AAY97175	Aay97175	Human FGF
35	1139	99.6	497	3	AAY97174	Aay97174	Human FGF
36	1139	99.6	497	3	AAY97172	Aay97172	Human FGF
37	1139	99.6	525	3	AAY97171	Aay97171	Human FGF
38	1139	99.6	525	3	AAY97173	Aay97173	Human FGF
39	1139	99.6	622	3	AAY97170	Aay97170	Human FGF
40	1139	99.6	729	9	ADZ12919	Adz12919	Human can
41	1139	99.6	731	2	AAR21686	Aar21686	Human bFG
42	1139	99.6	764	3	AAB58376	Aab58376	Lung canc
43	1139	99.6	783	8	ABM83106	Abm83106	Human dia
44	1139	99.6	820	2	AAR47233	Aar47233	Human fib
45	1139	99.6	820	4	AAB84383	Aab84383	Amino aci

OM protein - protein search, using sw model

Run on: February 16, 2006, 20:46:07 ; Search time 144.563 Seconds
                                            (without alignments)
                                            609.853 Million cell updates/sec

Title: US-10-049-429-1
Perfect score: 1144
Sequence: 1 MPVAPYWTSPEKMEKKLHAV.........TCLAGNSIGLSHHSAWLTVL 211

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_AA_Main:*
                 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
                 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
                 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
                 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
                 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
                 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                   %
Result   Query
   No.   Score Match Length DB ID   Description
----
     1   1144 100.0   609 4 US-10-087-192-384   Sequence 384, App
     2   1144 100.0   662 5 US-10-868-577A-60   Sequence 60, Appl
     3   1144 100.0   702 3 US-09-805-020-47   Sequence 47, Appl
     4   1144 100.0   759 5 US-10-941-486-9   Sequence 9, Appli
     5   1144 100.0   822 4 US-10-204-041-2   Sequence 2, Appli
     6   1144 100.0   822 4 US-10-394-322A-26   Sequence 26, Appl
     7   1144 100.0   822 4 US-10-307-817-8   Sequence 8, Appli
     8   1144 100.0   822 5 US-10-723-860-475   Sequence 475, App
     9   1144 100.0   822 5 US-10-285-405-3   Sequence 3, Appli
    10   1144 100.0   822 5 US-10-287-436A-508   Sequence 508, App
    11   1144 100.0   822 5 US-10-287-436A-511   Sequence 511, App

12	1144	100.0	822	5	US-10-287-436A-1201	Sequence 1201, Ap
13	1144	100.0	822	5	US-10-287-436A-1202	Sequence 1202, Ap
14	1139	99.6	451	4	US-10-087-192-381	Sequence 381, App
15	1139	99.6	488	4	US-10-683-255-12	Sequence 12, Appl
16	1139	99.6	497	4	US-10-683-255-6	Sequence 6, Appli
17	1139	99.6	497	4	US-10-683-255-10	Sequence 10, Appl
18	1139	99.6	525	4	US-10-683-255-4	Sequence 4, Appli
19	1139	99.6	525	4	US-10-683-255-8	Sequence 8, Appli
20	1139	99.6	622	4	US-10-683-255-2	Sequence 2, Appli
21	1139	99.6	764	3	US-09-925-302-714	Sequence 714, App
22	1139	99.6	764	3	US-09-925-302-714	Sequence 714, App
23	1139	99.6	820	6	US-11-037-713-16	Sequence 16, Appl
24	1138	99.5	225	6	US-11-021-951-158	Sequence 158, App
25	1135	99.2	822	3	US-09-757-415A-2	Sequence 2, Appli
26	1133	99.0	820	4	US-10-302-812-42	Sequence 42, Appl
27	1133	99.0	820	5	US-10-482-029-164	Sequence 164, App
28	997	87.2	735	4	US-10-307-817-6	Sequence 6, Appli
29	997	87.2	824	4	US-10-307-817-4	Sequence 4, Appli
30	938	82.0	216	6	US-11-021-951-159	Sequence 159, App
31	938	82.0	471	4	US-10-087-192-1134	Sequence 1134, Ap
32	938	82.0	732	6	US-11-019-829-109	Sequence 109, App
33	938	82.0	768	6	US-11-019-829-104	Sequence 104, App
34	938	82.0	821	4	US-10-394-322A-27	Sequence 27, Appl
35	938	82.0	821	4	US-10-302-812-44	Sequence 44, Appl
36	938	82.0	821	5	US-10-941-486-8	Sequence 8, Appli
37	938	82.0	821	6	US-11-019-829-99	Sequence 99, Appl
38	926.5	81.0	788	6	US-11-019-829-108	Sequence 108, App
39	926.5	81.0	822	6	US-11-019-829-103	Sequence 103, App
40	893	78.1	377	4	US-10-389-821-22	Sequence 22, Appl
41	893	78.1	806	4	US-10-394-322A-28	Sequence 28, Appl
42	893	78.1	806	4	US-10-403-161-58	Sequence 58, Appl
43	893	78.1	806	5	US-10-696-639-42	Sequence 42, Appl
44	893	78.1	806	5	US-10-941-486-7	Sequence 7, Appli
45	893	78.1	806	5	US-10-734-661A-1	Sequence 1, Appli

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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 20, 2006, 02:26:52 ; Search time 4845 Seconds
                                          (without alignments)
                                          2475.535 Million cell updates/sec

Title: US-10-049-429-1
Perfect score: 1144
Sequence: 1 MPVAPYWTSPEKMEKKLHAV.........TCLAGNSIGLSHHSAWLTVL 211

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10049429/runat_17022006_170938_8118/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=45 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02h
-USER=US10049429_@CGN_1_1_4939_@runat_17022006_170938_8118 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   GenEmbl:*
                 1: gb_ba:*
                 2: gb_in:*
                 3: gb_env:*
                 4: gb_om:*
                 5: gb_ov:*
                 6: gb_pat:*
                 7: gb_ph:*
                 8: gb_pr:*
                 9: gb_ro:*
                 10: gb_sts:*
                 11: gb_sy:*
                 12: gb_un:*
                 13: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1144	100.0	864	6	AX040410	AX040410 Sequence
2	1144	100.0	1607	6	CQ720744	CQ720744 Sequence
3	1144	100.0	2366	8	HSFGR2IGA	X57119 Human mRNA
4	1144	100.0	2469	6	A29216	A29216 H.sapiens D
5	1144	100.0	2469	6	I66313	I66313 Sequence 1
6	1144	100.0	2469	6	AX481457	AX481457 Sequence
7	1144	100.0	2633	8	HSFGR3IGA	X57121 Human mRNA
8	1144	100.0	2662	6	CQ793703	CQ793703 Sequence
9	1144	100.0	2662	6	AX601391	AX601391 Sequence
10	1144	100.0	2662	8	HSFGFRFL	X52833 Human flg m
11	1144	100.0	2733	6	AR019675	AR019675 Sequence
12	1144	100.0	2733	8	HSFGFR	X51803 Human mRNA
13	1144	100.0	3365	8	HUMFGF2H	M34185 Human fibro
14	1144	100.0	3525	6	E03799	E03799 cDNA sequen
15	1144	100.0	3913	8	BC015035	BC015035 Homo sapi
16	1144	100.0	3981	8	HSNSAMTK	X66945 H.sapiens N
17	1144	100.0	4049	6	CS032815	CS032815 Sequence
18	1144	100.0	4049	6	CS041767	CS041767 Sequence
19	1144	100.0	4157	8	AB208919	AB208919 Homo sapi
20	1140	99.7	1608	8	HUMHBGFC	M63889 Human hepar
21	1140	99.7	3198	8	HUMHBGFA	M63887 Human hepar
22	1140	99.7	3223	8	HUMHBGFBV	M63888 Human hepar
23	1140	99.7	4066	6	AX587712	AX587712 Sequence
24	1139	99.6	1467	6	AR435734	AR435734 Sequence
25	1139	99.6	1494	6	AR435731	AR435731 Sequence
26	1139	99.6	1494	6	AR435733	AR435733 Sequence
27	1139	99.6	1578	6	AR435730	AR435730 Sequence
28	1139	99.6	1578	6	AR435732	AR435732 Sequence
29	1139	99.6	1869	6	AR435729	AR435729 Sequence
30	1139	99.6	2360	6	AR380743	AR380743 Sequence
31	1139	99.6	2360	8	HSFGR2IG	X57122 Human mRNA
32	1139	99.6	2625	9	MMFGF	X51893 Mouse fms-1
33	1139	99.6	2627	8	HSFGR3IG	X57120 Human mRNA
34	1139	99.6	2877	9	BC033447	BC033447 Mus muscu
35	1139	99.6	3195	8	BC091494	BC091494 Homo sapi
36	1139	99.6	3328	6	E03335	E03335 Human b-FGF
37	1139	99.6	3328	6	AX774782	AX774782 Sequence
38	1139	99.6	3328	8	HUMBFGFS	M37722 Human short
39	1139	99.6	3850	9	BC010200	BC010200 Mus muscu
40	1139	99.6	3901	8	HUMFGFAA	M60485 Human fibro
41	1135	99.2	2259	9	MMU23445	U23445 Mus musculu
42	1135	99.2	2526	6	BD016930	BD016930 Antisense
43	1135	99.2	2526	9	MMU22324	U22324 Mus musculu
44	1135	99.2	3503	8	HUMFGF3H	M34186 Human fibro
45	1134	99.1	789	6	AX040412	AX040412 Sequence

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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 17, 2006, 08:09:24 ; Search time 199.927 Seconds
                                              (without alignments)
                                              1876.011 Million cell updates/sec

Title: US-10-049-429-1
Perfect score: 1144
Sequence: 1 MPVAPYWTSPEKMEKKLHAV.........TCLAGNSIGLSHHSAWLTVL 211

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10049429/runat_16022006_105609_6342/app_query.fasta_1
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss07 -USER=US10049429_@CGN_1_1_237_@runat_16022006_105609_6342 -NCPU=6
-ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Issued_Patents_NA:*
                 1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
                 2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
                 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                 5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
                 6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                 7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
                 8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
                 9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1144	100.0	2469	2	US-07-997-133-2	Sequence 2, Appli
2	1144	100.0	2469	2	US-08-459-296-1	Sequence 1, Appli
3	1144	100.0	2469	6	US-07-997-133-2	Sequence 2, Appli
4	1144	100.0	2662	2	US-08-451-822A-14	Sequence 14, Appl
5	1144	100.0	2662	3	US-08-323-430-14	Sequence 14, Appl
6	1144	100.0	2733	2	US-08-371-001-14	Sequence 14, Appl
7	1144	100.0	2733	6	PCT-US96-00331-14	Sequence 14, Appl
8	1144	100.0	3944	3	US-09-949-016-1876	Sequence 1876, Ap
9	1144	100.0	3944	3	US-09-949-016-1877	Sequence 1877, Ap
10	1144	100.0	3944	3	US-09-949-016-1878	Sequence 1878, Ap
11	1144	100.0	3944	3	US-09-949-016-1879	Sequence 1879, Ap
12	1144	100.0	3944	3	US-09-949-016-1880	Sequence 1880, Ap
13	1144	100.0	3944	3	US-09-949-016-1881	Sequence 1881, Ap
14	1144	100.0	3944	3	US-09-949-016-1882	Sequence 1882, Ap
15	1144	100.0	3944	3	US-09-949-016-1883	Sequence 1883, Ap
16	1139	99.6	1467	3	US-09-499-846-11	Sequence 11, Appl
17	1139	99.6	1494	3	US-09-499-846-5	Sequence 5, Appli
18	1139	99.6	1494	3	US-09-499-846-9	Sequence 9, Appli
19	1139	99.6	1578	3	US-09-499-846-3	Sequence 3, Appli
20	1139	99.6	1578	3	US-09-499-846-7	Sequence 7, Appli
21	1139	99.6	1869	3	US-09-499-846-1	Sequence 1, Appli
22	1139	99.6	1983	3	US-09-057-860A-8	Sequence 8, Appli
23	1139	99.6	2360	3	US-09-023-655-1288	Sequence 1288, Ap
24	1119	97.8	3503	2	US-07-631-717A-1	Sequence 1, Appli
25	1119	97.8	3503	2	US-08-166-717D-1	Sequence 1, Appli
26	938	82.0	2079	3	US-09-949-016-3171	Sequence 3171, Ap
27	938	82.0	2079	3	US-09-949-016-3172	Sequence 3172, Ap
28	938	82.0	2079	3	US-09-949-016-3173	Sequence 3173, Ap
29	938	82.0	2079	3	US-09-949-016-3174	Sequence 3174, Ap
30	938	82.0	2079	3	US-09-949-016-3175	Sequence 3175, Ap
31	938	82.0	2079	3	US-09-949-016-3176	Sequence 3176, Ap
32	938	82.0	2079	3	US-09-949-016-3177	Sequence 3177, Ap
33	938	82.0	2079	3	US-09-949-016-3178	Sequence 3178, Ap
34	938	82.0	2079	3	US-09-949-016-3179	Sequence 3179, Ap
35	938	82.0	2079	3	US-09-949-016-3180	Sequence 3180, Ap
36	938	82.0	3416	2	US-08-451-822A-15	Sequence 15, Appl
37	938	82.0	3416	3	US-08-323-430-15	Sequence 15, Appl
38	938	82.0	4268	3	US-09-954-556-3	Sequence 3, Appli
39	924	80.8	3306	3	US-09-954-556-10	Sequence 10, Appl
40	907	79.3	2675	2	US-08-070-165F-5	Sequence 5, Appli
41	907	79.3	2675	2	US-08-885-418-5	Sequence 5, Appli
42	898.5	78.5	2587	3	US-09-949-016-3321	Sequence 3321, Ap
43	898.5	78.5	2587	3	US-09-949-016-3322	Sequence 3322, Ap
44	898.5	78.5	2587	3	US-09-949-016-3323	Sequence 3323, Ap
45	898.5	78.5	2587	3	US-09-949-016-3324	Sequence 3324, Ap

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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 17, 2006, 12:45:19 ; Search time 444.146 Seconds
                                               (without alignments)
                                               1008.448 Million cell updates/sec

Title: US-10-049-429-1
Perfect score: 1144
Sequence: 1 MPVAPYWTSPEKMEKKLHAV.........TCLAGNSIGLSHHSAWLTVL 211

Scoring table: BLOSUM62
                  Xgapop 10.0 , Xgapext 0.5
                  Ygapop 10.0 , Ygapext 0.5
                  Fgapop 6.0 , Fgapext 7.0
                  Delop   6.0 , Delext   7.0

Searched: 7204252 seqs, 1061369211 residues

Total number of hits satisfying chosen parameters: 14408504

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10049429/runat_16022006_105622_6651/app_query.fasta_1
-DB=Published_Applications_NA_New -QFMT=fastap -SUFFIX=rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss02h
-USER=US10049429_@CGN_1_1_380_@runat_16022006_105622_6651 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Published_Applications_NA_New:*
                  1: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
                  2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
                  3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                  4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                  5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
                  6: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq1:*
                  7: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
                  8: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq1:*
                  9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
                  10: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
                  11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3:*

```
12:  /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq4:*
13:  /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1127	98.5	2469	12	US-11-136-527-319	Sequence 319, App
2	892	78.0	3286	12	US-11-136-527-158	Sequence 158, App
3	830	72.6	4574	9	US-11-072-175-132	Sequence 132, App
4	813	71.1	2648	12	US-11-136-527-220	Sequence 220, App
5	791	69.1	2672	12	US-11-136-527-3514	Sequence 3514, Ap
6	768	67.1	2311	12	US-11-136-527-3513	Sequence 3513, Ap
7	270	23.6	698	8	US-10-750-185-28032	Sequence 28032, A
8	270	23.6	698	8	US-10-750-623-28032	Sequence 28032, A
9	230	20.1	15660	8	US-10-453-372-1001	Sequence 1001, Ap
10	230	20.1	18209	12	US-11-065-695-19	Sequence 19, Appl
11	207	18.1	2462	9	US-11-072-512-78	Sequence 78, Appl
12	205	17.9	2220	9	US-11-072-512-1739	Sequence 1739, Ap
13	201.5	17.6	3413	12	US-11-136-527-2290	Sequence 2290, Ap
14	201.5	17.6	3757	12	US-11-091-883-86	Sequence 86, Appl
c 15	201.5	17.6	3903	12	US-11-091-883-87	Sequence 87, Appl
c 16	201.5	17.6	4564	8	US-10-821-234-40	Sequence 40, Appl
17	201	17.6	6691	12	US-11-091-883-199	Sequence 199, App
18	198.5	17.4	5110	12	US-11-136-527-2160	Sequence 2160, Ap
19	195	17.0	1975	8	US-10-453-372-723	Sequence 723, App
20	195	17.0	2011	8	US-10-453-372-669	Sequence 669, App
21	195	17.0	2011	8	US-10-453-372-681	Sequence 681, App
22	195	17.0	2011	8	US-10-453-372-721	Sequence 721, App
23	195	17.0	2059	8	US-10-453-372-679	Sequence 679, App
24	195	17.0	2256	9	US-11-072-512-1425	Sequence 1425, Ap
25	195	17.0	2902	8	US-10-453-372-711	Sequence 711, App
26	195	17.0	2902	8	US-10-453-372-713	Sequence 713, App
27	195	17.0	2902	8	US-10-453-372-725	Sequence 725, App
28	195	17.0	2902	8	US-10-453-372-727	Sequence 727, App
29	195	17.0	7876	8	US-10-453-372-665	Sequence 665, App
30	195	17.0	7876	8	US-10-453-372-731	Sequence 731, App
31	195	17.0	7876	8	US-10-453-372-733	Sequence 733, App
32	195	17.0	7876	8	US-10-453-372-735	Sequence 735, App
33	195	17.0	7876	8	US-10-453-372-737	Sequence 737, App
34	195	17.0	7876	8	US-10-453-372-739	Sequence 739, App
35	195	17.0	7876	8	US-10-453-372-741	Sequence 741, App
36	195	17.0	7876	8	US-10-453-372-743	Sequence 743, App
37	195	17.0	7876	8	US-10-453-372-745	Sequence 745, App
38	195	17.0	7876	8	US-10-453-372-747	Sequence 747, App
39	195	17.0	7876	8	US-10-453-372-749	Sequence 749, App
40	194.5	17.0	9645	12	US-11-186-284-48	Sequence 48, Appl
41	194.5	17.0	9646	12	US-11-080-991-53	Sequence 53, Appl
42	193	16.9	3333	8	US-10-453-372-1083	Sequence 1083, Ap
43	193	16.9	4762	8	US-10-453-372-1087	Sequence 1087, Ap
44	193	16.9	4956	12	US-11-136-527-2620	Sequence 2620, Ap
45	193	16.9	5101	8	US-10-453-372-1085	Sequence 1085, Ap

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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 17, 2006, 07:55:47 ; Search time 4463.6 Seconds
                                              (without alignments)
                                              2211.683 Million cell updates/sec

Title: US-10-049-429-1
Perfect score: 1144
Sequence: 1 MPVAPYWTSPEKMEKKLHAV..........TCLAGNSIGLSHHSAWLTVL 211

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10049429/runat_16022006_105607_6293/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02h
-USER=US10049429_@CGN_1_1_6731_@runat_16022006_105607_6293 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   EST:*
                 1: gb_est1:*
                 2: gb_est2:*
                 3: gb_est3:*
                 4: gb_htc:*
                 5: gb_est4:*
                 6: gb_est5:*
                 7: gb_est6:*
                 8: gb_est7:*
                 9: gb_gss1:*
                 10: gb_gss2:*
                 11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

<p align="center">SUMMARIES</p>

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1139	99.6	778	6	CB247698	CB247698 UI-M-FIO-
2	1139	99.6	783	3	BQ179450	BQ179450 UI-M-EWO-
3	1139	99.6	821	8	CX563627	CX563627 UI-M-IBO-
4	1139	99.6	833	8	CX568904	CX568904 UI-M-IBO-
5	1139	99.6	3259	4	AK028354	AK028354 Mus muscu
6	1139	99.6	3513	4	CR859698	CR859698 Pongo pyg
7	1132	99.0	734	7	CN333264	CN333264 170005325
8	1131	98.9	868	7	CK020755	CK020755 AGENCOURT
9	1126	98.4	729	5	BQ768898	BQ768898 UI-M-FCO-
10	1119	97.8	768	1	AU124659	AU124659 AU124659
11	1117	97.6	877	1	AU132315	AU132315 AU132315
12	1114	97.4	801	1	AU121630	AU121630 AU121630
13	1112	97.2	765	1	AU125277	AU125277 AU125277
14	1105.5	96.6	4050	4	AK049704	AK049704 Mus muscu
15	1088.5	95.1	727	1	AU123613	AU123613 AU123613
16	1087	95.0	660	3	BI657685	BI657685 603281259
17	1085	94.8	698	7	CN333307	CN333307 170005326
18	1071	93.6	667	1	AU123382	AU123382 AU123382
19	1070	93.5	857	7	CO248161	CO248161 AGENCOURT
20	1063	92.9	787	7	CO246239	CO246239 AGENCOURT
21	1062.5	92.9	696	6	CF125910	CF125910 UI-HF-ELO
22	1055	92.2	727	6	CF125008	CF125008 UI-HF-ELO
23	1053	92.0	973	2	BF981311	BF981311 602308558
24	1049	91.7	836	7	CO405524	CO405524 AGENCOURT
25	1038	90.7	877	6	CD557306	CD557306 AGENCOURT
26	1037	90.6	674	1	AU123364	AU123364 AU123364
27	1037	90.6	771	8	CX217340	CX217340 MNS31316
28	1018	89.0	774	7	CK480651	CK480651 AGENCOURT
29	1017	88.9	761	3	BQ180144	BQ180144 UI-M-EWO-
30	1008	88.1	720	2	BF168524	BF168524 601775424
31	1008	88.1	755	7	CN333282	CN333282 170005999
32	1007	88.0	865	5	BX390662	BX390662 BX390662
33	1003	87.7	761	5	BU320732	BU320732 603854853
34	988	86.4	562	1	AU279800	AU279800 AU279800
35	988	86.4	679	6	CF125963	CF125963 UI-HF-ELO
36	981	85.8	907	7	CK022877	CK022877 AGENCOURT
37	961	84.0	752	8	CX474004	CX474004 JGI_XZG49
38	956	83.6	901	8	CX375663	CX375663 JGI_XZT59
39	954	83.4	815	8	CX966008	CX966008 JGI_CAAP1
40	953	83.3	873	8	CX490517	CX490517 JGI_XZG33
41	952	83.2	677	2	BE612660	BE612660 601452506
42	940	82.2	652	6	CF126009	CF126009 UI-HF-ELO
43	939	82.1	740	7	CK636063	CK636063 UI-M-HNO-
44	939	82.1	772	7	CO556760	CO556760 AGENCOURT
45	938	82.0	2460	11	DQ037912	DQ037912 Homo sapi

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OM protein - protein search, using sw model

Run on: February 18, 2006, 14:52:30 ; Search time 47 Seconds
                                          (without alignments)
                                          371.161 Million cell updates/sec

Title: US-10-049-429-1
Perfect score: 1144
Sequence: 1 MPVAPYWTSPEKMEKKLHAV.........TCLAGNSIGLSHHSAWLTVL 211

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_AA:*
                 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
                 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
                 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
                 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
  No.   Score   Match Length DB   ID   Description
----
     1   1144   100.0   609 2   US-09-949-016-7747   Sequence 7747, Ap
     2   1144   100.0   609 2   US-09-949-016-7748   Sequence 7748, Ap
     3   1144   100.0   609 2   US-09-949-016-7749   Sequence 7749, Ap
     4   1144   100.0   609 2   US-09-949-016-7750   Sequence 7750, Ap
     5   1144   100.0   609 2   US-09-949-016-7751   Sequence 7751, Ap
     6   1144   100.0   609 2   US-09-949-016-7752   Sequence 7752, Ap
     7   1144   100.0   609 2   US-09-949-016-7753   Sequence 7753, Ap
     8   1144   100.0   609 2   US-09-949-016-7754   Sequence 7754, Ap
     9   1144   100.0   733 1   US-07-640-029-4   Sequence 4, Appli
    10   1144   100.0   733 1   US-07-921-807B-6   Sequence 6, Appli
    11   1144   100.0   733 1   US-08-441-944A-6   Sequence 6, Appli

12	1144	100.0	733	2	US-08-439-992A-4	Sequence 4, Appli
13	1144	100.0	733	2	US-09-620-561-4	Sequence 4, Appli
14	1144	100.0	817	1	US-07-640-029-2	Sequence 2, Appli
15	1144	100.0	822	1	US-07-997-133-1	Sequence 1, Appli
16	1144	100.0	822	1	US-07-921-807B-4	Sequence 4, Appli
17	1144	100.0	822	1	US-08-459-296-2	Sequence 2, Appli
18	1144	100.0	822	1	US-08-441-944A-4	Sequence 4, Appli
19	1144	100.0	822	1	US-08-451-822A-12	Sequence 12, Appl
20	1144	100.0	822	2	US-08-439-992A-2	Sequence 2, Appli
21	1144	100.0	822	2	US-08-323-430-12	Sequence 12, Appl
22	1144	100.0	822	2	US-09-620-561-2	Sequence 2, Appli
23	1139	99.6	351	4	PCT-US93-05703-2	Sequence 2, Appli
24	1139	99.6	488	2	US-09-499-846-12	Sequence 12, Appl
25	1139	99.6	497	2	US-09-499-846-6	Sequence 6, Appli
26	1139	99.6	497	2	US-09-499-846-10	Sequence 10, Appl
27	1139	99.6	525	2	US-09-499-846-4	Sequence 4, Appli
28	1139	99.6	525	2	US-09-499-846-8	Sequence 8, Appli
29	1139	99.6	622	2	US-09-499-846-2	Sequence 2, Appli
30	1139	99.6	820	1	US-07-921-807B-3	Sequence 3, Appli
31	1139	99.6	820	1	US-08-441-944A-3	Sequence 3, Appli
32	1139	99.6	820	2	US-08-439-992A-1	Sequence 1, Appli
33	1139	99.6	820	2	US-09-620-561-1	Sequence 1, Appli
34	1135	99.2	731	1	US-07-921-807B-5	Sequence 5, Appli
35	1135	99.2	731	1	US-08-441-944A-5	Sequence 5, Appli
36	1135	99.2	731	2	US-08-439-992A-3	Sequence 3, Appli
37	1135	99.2	731	2	US-09-620-561-3	Sequence 3, Appli
38	1115	97.5	729	1	US-07-640-029-3	Sequence 3, Appli
39	1110	97.0	820	1	US-08-166-717D-6	Sequence 6, Appli
40	1107.5	96.8	816	1	US-07-640-029-1	Sequence 1, Appli
41	938	82.0	471	2	US-09-949-016-9042	Sequence 9042, Ap
42	938	82.0	471	2	US-09-949-016-9043	Sequence 9043, Ap
43	938	82.0	471	2	US-09-949-016-9044	Sequence 9044, Ap
44	938	82.0	471	2	US-09-949-016-9045	Sequence 9045, Ap
45	938	82.0	471	2	US-09-949-016-9046	Sequence 9046, Ap

OM protein - protein search, using sw model

Run on: February 16, 2006, 20:46:52 ; Search time 13.5335 Seconds
                                              (without alignments)
                                              221.619 Million cell updates/sec

Title: US-10-049-429-1
Perfect score: 1144
Sequence: 1 MPVAPYWTSPEKMEKKLHAV..........TCLAGNSIGLSHHSAWLTVL 211

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 107819 seqs, 14214640 residues

Total number of hits satisfying chosen parameters: 107819

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_AA_New:*
                 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
                 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
                 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
                 4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
                 5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
                 6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
                 7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
                 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.

                                    SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1135	99.2	822	7	US-11-183-567A-2	Sequence 2, Appli
2	830	72.6	822	7	US-11-072-175-254	Sequence 254, App
3	352.5	30.8	438	7	US-11-186-541-2	Sequence 2, Appli
4	352.5	30.8	504	7	US-11-186-541-3	Sequence 3, Appli
5	352.5	30.8	529	7	US-11-186-541-1	Sequence 1, Appli
6	230	20.1	4495	6	US-10-453-372-1002	Sequence 1002, Ap
7	230	20.1	5636	7	US-11-065-695-20	Sequence 20, Appl
8	207	18.1	619	7	US-11-072-512-2048	Sequence 2048, Ap
9	205	17.9	329	7	US-11-072-512-3709	Sequence 3709, Ap

10	201.5	17.6	409	6	US-10-821-234-892	Sequence 892, App
11	195	17.0	650	7	US-11-072-512-3395	Sequence 3395, Ap
12	195	17.0	652	6	US-10-453-372-722	Sequence 722, App
13	195	17.0	652	6	US-10-453-372-724	Sequence 724, App
14	195	17.0	670	6	US-10-453-372-670	Sequence 670, App
15	195	17.0	670	6	US-10-453-372-682	Sequence 682, App
16	195	17.0	686	6	US-10-453-372-680	Sequence 680, App
17	195	17.0	961	6	US-10-453-372-726	Sequence 726, App
18	195	17.0	961	6	US-10-453-372-728	Sequence 728, App
19	195	17.0	967	6	US-10-453-372-712	Sequence 712, App
20	195	17.0	967	6	US-10-453-372-714	Sequence 714, App
21	195	17.0	2617	6	US-10-453-372-666	Sequence 666, App
22	195	17.0	2617	6	US-10-453-372-732	Sequence 732, App
23	195	17.0	2617	6	US-10-453-372-734	Sequence 734, App
24	195	17.0	2617	6	US-10-453-372-736	Sequence 736, App
25	195	17.0	2617	6	US-10-453-372-738	Sequence 738, App
26	195	17.0	2617	6	US-10-453-372-740	Sequence 740, App
27	195	17.0	2617	6	US-10-453-372-742	Sequence 742, App
28	195	17.0	2617	6	US-10-453-372-744	Sequence 744, App
29	195	17.0	2617	6	US-10-453-372-746	Sequence 746, App
30	195	17.0	2617	6	US-10-453-372-748	Sequence 748, App
31	195	17.0	2617	6	US-10-453-372-750	Sequence 750, App
32	194.5	17.0	2828	7	US-11-080-991-54	Sequence 54, Appl
33	194.5	17.0	2828	7	US-11-186-284-49	Sequence 49, Appl
34	193	16.9	1068	6	US-10-453-372-1084	Sequence 1084, Ap
35	193	16.9	1077	6	US-10-453-372-1086	Sequence 1086, Ap
36	193	16.9	1093	6	US-10-453-372-1088	Sequence 1088, Ap
37	191	16.7	1068	6	US-10-453-372-1090	Sequence 1090, Ap
38	188.5	16.5	7968	7	US-11-186-731-5	Sequence 5, Appli
39	188	16.4	473	6	US-10-453-372-696	Sequence 696, App
40	187	16.3	670	6	US-10-453-372-710	Sequence 710, App
41	186	16.3	457	6	US-10-453-372-686	Sequence 686, App
42	186	16.3	457	6	US-10-453-372-690	Sequence 690, App
43	186	16.3	460	6	US-10-453-372-688	Sequence 688, App
44	186	16.3	473	6	US-10-453-372-684	Sequence 684, App
45	186	16.3	473	6	US-10-453-372-692	Sequence 692, App

```
                          GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on:            February 20, 2006, 02:42:37 ; Search time 587 Seconds
                                          (without alignments)
                                          2395.656 Million cell updates/sec


Title:            US-10-049-429-1
Perfect score:    1144
Sequence:         1 MPVAPYWTSPEKMEKKLHAV..........TCLAGNSIGLSHHSAWLTVL 211


Scoring table:    BLOSUM62
                  Xgapop 10.0 , Xgapext  0.5
                  Ygapop 10.0 , Ygapext  0.5
                  Fgapop  6.0 , Fgapext  7.0
                  Delop   6.0 , Delext   7.0


Searched:         4996997 seqs, 3332346308 residues


Total number of hits satisfying chosen parameters:       9993994


Minimum DB seq length: 0
Maximum DB seq length: 2000000000


Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries


Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10049429/runat_17022006_170939_8131/app_query.fasta_1
-DB=N_Geneseq -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=45 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02h
-USER=US10049429_@CGN_1_1_727_@runat_17022006_170939_8131 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7


Database :        N_Geneseq_21:*
                  1:  geneseqn1980s:*
                  2:  geneseqn1990s:*
                  3:  geneseqn2000s:*
                  4:  geneseqn2001as:*
                  5:  geneseqn2001bs:*
                  6:  geneseqn2002as:*
                  7:  geneseqn2002bs:*
                  8:  geneseqn2003as:*
                  9:  geneseqn2003bs:*
                  10:  geneseqn2003cs:*
                  11:  geneseqn2003ds:*
                  12:  geneseqn2004as:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                                    SUMMARIES

		% Query				
Result No.	Score	Match	Length	DB	ID	Description
1	1144	100.0	864	3	AAC66559	Aac66559 Human FGF
2	1144	100.0	2202	10	ADL13668	Adl13668 Osteoarth
3	1144	100.0	2469	2	AAQ13311	Aaq13311 Basic FGF
4	1144	100.0	2469	6	ABV78187	Abv78187 Human FGF
5	1144	100.0	2469	6	ABZ35763	Abz35763 Human FGF
6	1144	100.0	2469	6	ABX10006	Abx10006 Human FGF
7	1144	100.0	2469	6	ABL91728	Abl91728 Human pol
8	1144	100.0	2469	13	ADS18135	Ads18135 Human FGF
9	1144	100.0	2469	13	ADS18136	Ads18136 Human FGF
10	1144	100.0	2662	8	AAD52780	Aad52780 Human FGF
11	1144	100.0	2662	13	ADS18134	Ads18134 Human FGF
12	1144	100.0	2731	12	ADO42158	Ado42158 Human NOV
13	1144	100.0	2733	2	AAT31051	Aat31051 Human fib
14	1144	100.0	2733	10	ACC42967	Acc42967 Human Fib
15	1144	100.0	3365	10	ADL13667	Adl13667 Osteoarth
16	1144	100.0	3525	2	AAQ27658	Aaq27658 N-sam cDN
17	1144	100.0	3611	14	ADZ12914	Adz12914 Human can
18	1144	100.0	3722	14	ADZ12912	Adz12912 Human can
19	1144	100.0	3747	14	ADZ12922	Adz12922 Human can
20	1144	100.0	3782	13	ACF91623	Acf91623 Human SIR
21	1144	100.0	3938	13	ACF91629	Acf91629 Human SIR
22	1144	100.0	3944	11	ACN44103	Acn44103 Human mRN
23	1144	100.0	3981	11	ADP65620	Adp65620 Human N-s
24	1144	100.0	3981	11	ADP65618	Adp65618 Human N-s
25	1144	100.0	3981	12	ADQ17657	Adq17657 Human sof
26	1144	100.0	4049	11	ADP65062	Adp65062 Human fib
27	1144	100.0	4049	11	ADP65063	Adp65063 Human fib
28	1144	100.0	4049	13	ACF91621	Acf91621 Human SIR
29	1144	100.0	4049	14	ADY16515	Ady16515 DNA encod
30	1144	100.0	4444	12	ADQ22324	Adq22324 Human sof
31	1144	100.0	4452	14	ADZ12924	Adz12924 Human can
32	1144	100.0	4628	6	ABS65210	Abs65210 cDNA enco
33	1140	99.7	4066	6	ABV94191	Abv94191 Breast ca
34	1140	99.7	4066	13	ADP24446	Adp24446 PRO polyp
35	1140	99.7	4066	13	ACF91627	Acf91627 Human SIR
36	1139	99.6	837	3	AAZ87249	Aaz87249 DNAencodi
37	1139	99.6	1467	3	AAA52132	Aaa52132 Human FGF
38	1139	99.6	1494	3	AAA52131	Aaa52131 Human FGF
39	1139	99.6	1494	3	AAA52129	Aaa52129 Human FGF
40	1139	99.6	1578	3	AAA52128	Aaa52128 Human FGF
41	1139	99.6	1578	3	AAA52130	Aaa52130 Human FGF
42	1139	99.6	1726	11	ACN44101	Acn44101 Mouse mRN
43	1139	99.6	1869	3	AAA52127	Aaa52127 Human FGF
44	1139	99.6	1983	5	AAD16027	Aad16027 Mouse sol
45	1139	99.6	2360	11	ADI31962	Adi31962 Human cDN

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 17, 2006, 12:27:39 ; Search time 882.14 Seconds
                                              (without alignments)
                                              1977.961 Million cell updates/sec

Title: US-10-049-429-1
Perfect score: 1144
Sequence: 1 MPVAPYWTSPEKMEKKLHAV..........TCLAGNSIGLSHHSAWLTVL 211

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10049429/runat_16022006_105619_6597/app_query.fasta_1
-DB=Published_Applications_NA_Main -QFMT=fastap -SUFFIX=rnpbm -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss02h
-USER=US10049429_@CGN_1_1_1364_@runat_16022006_105619_6597 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Published_Applications_NA_Main:*
                 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
                 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
                 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
                 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
                 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
                 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
                 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
                 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
                 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
                 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1144	100.0	2469	7	US-10-384-339C-71	Sequence 71, Appl
2	1144	100.0	2662	6	US-10-204-041-1	Sequence 1, Appli
3	1144	100.0	2731	7	US-10-307-817-7	Sequence 7, Appli
4	1144	100.0	2733	9	US-10-285-405-4	Sequence 4, Appli
5	1144	100.0	3944	5	US-10-087-192-383	Sequence 383, App
6	1144	100.0	3981	8	US-10-723-860-474	Sequence 474, App
7	1144	100.0	3981	9	US-10-287-436A-770	Sequence 770, App
8	1144	100.0	4049	9	US-10-287-436A-156	Sequence 156, App
9	1144	100.0	4049	9	US-10-287-436A-159	Sequence 159, App
10	1144	100.0	4444	8	US-10-723-860-5144	Sequence 5144, Ap
11	1144	100.0	4628	3	US-09-805-020-11	Sequence 11, Appl
12	1140	99.7	4066	6	US-10-007-926A-182	Sequence 182, App
13	1140	99.7	4066	6	US-10-159-563-305	Sequence 305, App
14	1139	99.6	1467	7	US-10-683-255-11	Sequence 11, Appl
15	1139	99.6	1494	7	US-10-683-255-5	Sequence 5, Appli
16	1139	99.6	1494	7	US-10-683-255-9	Sequence 9, Appli
17	1139	99.6	1578	7	US-10-683-255-3	Sequence 3, Appli
18	1139	99.6	1578	7	US-10-683-255-7	Sequence 7, Appli
19	1139	99.6	1726	5	US-10-087-192-380	Sequence 380, App
20	1139	99.6	1869	7	US-10-683-255-1	Sequence 1, Appli
21	1139	99.6	2360	7	US-10-641-643-1288	Sequence 1288, Ap
22	1139	99.6	3328	6	US-10-101-510-299	Sequence 299, App
23	1139	99.6	3328	7	US-10-283-975A-98	Sequence 98, Appl
24	1139	99.6	3454	5	US-10-044-090-48	Sequence 48, Appl
25	1139	99.6	3726	3	US-09-925-302-271	Sequence 271, App
26	1139	99.6	3726	3	US-09-925-302-271	Sequence 271, App
27	1139	99.6	3786	9	US-10-956-157-2426	Sequence 2426, Ap
28	1139	99.6	5438	8	US-10-723-860-5897	Sequence 5897, Ap
29	1133	99.0	3343	7	US-10-302-812-41	Sequence 41, Appl
30	1133	99.0	3343	8	US-10-482-029-163	Sequence 163, App
31	1133	99.0	3343	9	US-10-287-436A-769	Sequence 769, App
32	1127	98.5	2469	7	US-10-664-705-12	Sequence 12, Appl
33	1029	89.9	1451	3	US-09-917-800A-1466	Sequence 1466, Ap
34	997	87.2	2470	7	US-10-307-817-5	Sequence 5, Appli
35	997	87.2	2737	7	US-10-307-817-3	Sequence 3, Appli
36	938	82.0	2079	5	US-10-087-192-1133	Sequence 1133, Ap
37	938	82.0	2466	7	US-10-384-339C-85	Sequence 85, Appl
38	938	82.0	3216	10	US-11-019-829-43	Sequence 43, Appl
39	938	82.0	3248	7	US-10-302-812-43	Sequence 43, Appl
40	938	82.0	4268	3	US-09-954-456-293	Sequence 293, App
41	938	82.0	4268	3	US-09-954-456-1599	Sequence 1599, Ap
42	938	82.0	4268	3	US-09-954-556-3	Sequence 3, Appli
43	938	82.0	4268	3	US-09-968-007A-461	Sequence 461, App
44	938	82.0	4268	9	US-10-843-641A-3320	Sequence 3320, Ap
45	938	82.0	4268	9	US-10-843-641A-4626	Sequence 4626, Ap

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OM protein - protein search, using sw model

Run on: February 16, 2006, 20:25:36 ; Search time 30.1429 Seconds
                                              (without alignments)
                                              673.517 Million cell updates/sec

Title: US-10-049-429-1
Perfect score: 1144
Sequence: 1 MPVAPYWTSPEKMEKKLHAV..........TCLAGNSIGLSHHSAWLTVL 211

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_80:*
                 1: pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

| | | %
Query | | | | |
Result No.	Score	Match	Length	DB	ID	Description
1	1144	100.0	662	2	C40862	heparin-binding gr
2	1144	100.0	822	1	TVHUFG	fibroblast growth
3	1135	99.2	733	2	I49293	fibroblast growth
4	1135	99.2	822	2	I49289	fibroblast growth
5	1134	99.1	729	2	A56795	fibroblast growth
6	1127	98.5	822	2	S29840	fibroblast growth
7	1120	97.9	822	1	TVMSFG	fibroblast growth
8	1120	97.9	832	2	JH0393	fibroblast growth
9	1112	97.2	819	1	TVCHFG	fibroblast growth
10	1065	93.1	361	2	PN0020	fibroblast growth
11	1026	89.7	816	2	A49151	fibroblast growth
12	970	84.8	814	1	A39752	fibroblast growth
13	945	82.6	812	1	A36477	fibroblast growth

14	939	82.1	353	2	S51242	heparin-binding fi
15	938	82.0	821	1	TVHUF2	fibroblast growth
16	932	81.5	823	2	B35963	protein-tyrosine k
17	929	81.2	806	2	A35963	protein-tyrosine k
18	926	80.9	821	1	TVMSBK	fibroblast growth
19	912	79.7	820	2	S17295	fibroblast growth
20	907	79.3	748	2	S41050	fibroblast growth
21	903.5	79.0	302	2	C36464	fibroblast growth
22	895	78.2	800	2	A48991	heparin-binding gr
23	895	78.2	801	2	I55363	fibroblast growth
24	893	78.1	806	1	TVHUF3	fibroblast growth
25	891.5	77.9	824	2	S36439	fibroblast growth
26	886	77.4	800	1	TVHU2F	fibroblast growth
27	871	76.1	480	2	B56182	fibroblast growth
28	862	75.3	818	2	JC4058	fibroblast growth
29	855	74.7	797	2	S38579	fibroblast growth
30	844.5	73.8	829	2	JC4583	fibroblast growth
31	842	73.6	822	2	S19947	fibroblast growth
32	842	73.6	822	2	B49151	fibroblast growth
33	841	73.5	713	2	I50128	fibroblast growth
34	837.5	73.2	813	1	A49123	fibroblast growth
35	830	72.6	682	2	A35969	heparin-binding gr
36	830	72.6	707	2	A38429	keratinocyte growt
37	830	72.6	769	2	S16236	fibroblast growth
38	830	72.6	822	2	B54846	fibroblast growth
39	830	72.6	822	2	A45081	fibroblast growth
40	830	72.6	822	2	A41794	keratinocyte growt
41	826	72.2	707	2	A54846	fibroblast growth
42	823	71.9	824	2	S24108	protein-tyrosine k
43	808	70.6	750	2	S41051	fibroblast growth
44	801	70.0	802	1	TVHUF4	fibroblast growth
45	797	69.7	705	2	S51635	fibroblast growth

```
                          GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on:            February 16, 2006, 20:21:06 ; Search time 181.472 Seconds
                                              (without alignments)
                                   820.326 Million cell updates/sec

Title:           US-10-049-429-1
Perfect score:   1144
Sequence:        1 MPVAPYWTSPEKMEKKLHAV.........TCLAGNSIGLSHHSAWLTVL 211

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters:      2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       UniProt_05.80:*
                 1:  uniprot_sprot:*
                 2:  uniprot_trembl:*


      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.


                               SUMMARIES
                      %
Result             Query
   No.    Score    Match  Length  DB   ID                    Description
-------------------------------------------------------------------------------
     1    1144     100.0     814   2   Q59H40_HUMAN          Q59h40 homo sapien
     2    1144     100.0     822   1   FGFR1_HUMAN           P11362 homo sapien
     3    1139      99.6     731   2   Q5BJG2_HUMAN          Q5bjg2 homo sapien
     4    1139      99.6     731   2   Q8CFK8_MOUSE          Q8cfk8 mus musculu
     5    1139      99.6     820   2   Q5R8Q3_PONPY          Q5r8q3 pongo pygma
     6    1139      99.6     820   2   Q8CIM9_MOUSE          Q8cim9 mus musculu
     7    1139      99.6     822   1   FGFR1_MOUSE           P16092 mus musculu
     8    1135      99.2     733   2   Q60830_MOUSE          Q60830 mus musculu
     9    1135      99.2     822   2   Q60818_MOUSE          Q60818 mus musculu
    10    1134      99.1     729   2   Q63827_RAT            Q63827 rattus norv
    11    1133      99.0     820   2   Q53H63_HUMAN          Q53h63 homo sapien
    12    1132      99.0     279   2   Q9UD50_HUMAN          Q9ud50 homo sapien
    13    1127      98.5     822   1   FGFR1_RAT             Q04589 rattus norv
    14    1120      97.9     287   2   Q9QW80_9MURI          Q9qw80 mus sp. fib
    15    1120      97.9     376   2   Q9QW78_9MURI          Q9qw78 mus sp. fib
```

16	1112	97.2	819	1	FGFR1_CHICK	P21804	gallus gall
17	1065	93.1	360	2	Q61565_MOUSE	Q61565	mus musculu
18	1065	93.1	361	2	Q9QW79_9MURI	Q9qw79	mus sp. fib
19	1018	89.0	816	2	Q91285_PLEWA	Q91285	pleurodeles
20	992	86.7	733	2	Q9QZM7_MOUSE	Q9qzm7	mus musculu
21	970	84.8	814	2	Q91897_XENLA	Q91897	xenopus lae
22	951	83.1	810	2	Q9PS96_XENLA	Q9ps96	xenopus lae
23	945	82.6	812	1	FGFR1_XENLA	P22182	xenopus lae
24	941	82.3	782	2	Q9TTZ3_RABIT	Q9ttz3	oryctolagus
25	940	82.2	330	2	Q63241_RAT	Q63241	rattus norv
26	940	82.2	804	2	Q800Z1_BRARE	Q800z1	brachydanio
27	940	82.2	806	2	Q90Z00_BRARE	Q90z00	brachydanio
28	939	82.1	353	2	Q63242_RAT	Q63242	rattus norv
29	939	82.1	446	2	Q63237_RAT	Q63237	rattus norv
30	938	82.0	723	2	Q86YI4_HUMAN	Q86yi4	homo sapien
31	938	82.0	821	1	FGFR2_HUMAN	P21802	homo sapien
32	932	81.5	823	1	CEK3_CHICK	P18461	gallus gall
33	929	81.2	806	1	CEK2_CHICK	P18460	gallus gall
34	924	80.8	821	1	FGFR2_MOUSE	P21803	mus musculu
35	907	79.3	729	2	Q91147_NOTVI	Q91147	notophthalm
36	896	78.3	678	2	Q5XUI1_SHEEP	Q5xui1	ovis aries
37	895.5	78.3	300	2	Q53G05_HUMAN	Q53g05	homo sapien
38	895	78.2	782	2	Q61563_MOUSE	Q61563	mus musculu
39	895	78.2	800	2	Q7TSI8_MOUSE	Q7tsi8	mus musculu
40	895	78.2	801	1	FGFR3_MOUSE	Q61851	mus musculu
41	893	78.1	769	2	Q8NI15_HUMAN	Q8ni15	homo sapien
42	893	78.1	802	2	Q95M13_BOVIN	Q95m13	bos taurus
43	893	78.1	806	1	FGFR3_HUMAN	P22607	homo sapien
44	893	78.1	879	2	Q59FL9_HUMAN	Q59fl9	homo sapien
45	892	78.0	800	2	Q9JHX9_RAT	Q9jhx9	rattus norv

OM protein - protein search, using sw model

Run on: February 16, 2006, 20:20:36 ; Search time 100.443 Seconds
                                            (without alignments)
                                            577.421 Million cell updates/sec

Title: US-10-049-429-17
Perfect score: 712
Sequence: 1 PGNYKKPKLLYCSNGHFLRI..........PRTHYGQKAILFLPLPVSSD 132

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_21:*
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                 7: geneseqp2003bs:*
                 8: geneseqp2004s:*
                 9: geneseqp2005s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES

            %
Result   Query
   No.   Score   Match Length DB   ID   Description
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     3   680   95.5   140   2   AAR25914   Aar25914 Human aci
     4   680   95.5   140   2   AAR34497   Aar34497 Human aci
     5   680   95.5   140   2   AAR74647   Aar74647 Human rec
     6   680   95.5   140   2   AAW04806   Aaw04806 Human aci
     7   680   95.5   141   2   AAR10527   Aar10527 Human aci
     8   680   95.5   141   5   AAU76945   Aau76945 Human aci

9	680	95.5	141	5	AAO19992	Aao19992	Protein o
10	680	95.5	141	8	ADO55206	Ado55206	Human aci
11	680	95.5	151	2	AAR05789	Aar05789	Human aFG
12	680	95.5	154	2	AAW04805	Aaw04805	Human bet
13	680	95.5	154	2	AAW06816	Aaw06816	Human end
14	680	95.5	154	2	AAW75414	Aaw75414	Human bet
15	680	95.5	154	2	AAW92283	Aaw92283	Human bet
16	680	95.5	154	6	ABR63868	Abr63868	Thrombin
17	680	95.5	154	8	ADO55207	Ado55207	Processed
18	680	95.5	155	1	AAP70482	Aap70482	Sequence
19	680	95.5	155	1	AAP94037	Aap94037	Human aci
20	680	95.5	155	2	AAR70812	Aar70812	FGF-1. 3/
21	680	95.5	155	2	AAR80776	Aar80776	Fibroblas
22	680	95.5	155	2	AAW75711	Aaw75711	Fibroblas
23	680	95.5	155	2	AAW75415	Aaw75415	Human end
24	680	95.5	155	2	AAW53022	Aaw53022	Fibroblas
25	680	95.5	155	2	AAW92291	Aaw92291	Human end
26	680	95.5	155	2	AAY08584	Aay08584	Human FGF
27	680	95.5	155	3	AAY32333	Aay32333	Human fib
28	680	95.5	155	3	AAY90410	Aay90410	FGF-1, SE
29	680	95.5	155	3	AAB10297	Aab10297	Fibroblas
30	680	95.5	155	4	AAB50705	Aab50705	Human fib
31	680	95.5	155	4	AAB61661	Aab61661	FGF1 prot
32	680	95.5	155	4	AAB50298	Aab50298	Human fib
33	680	95.5	155	4	AAB50273	Aab50273	Human aci
34	680	95.5	155	4	AAB85812	Aab85812	Human fib
35	680	95.5	155	5	AAU76943	Aau76943	Human aci
36	680	95.5	155	5	AAO19990	Aao19990	Protein o
37	680	95.5	155	5	AAO19994	Aao19994	Protein o
38	680	95.5	155	5	ABB99120	Abb99120	Human fib
39	680	95.5	155	6	ABP54277	Abp54277	Human fib
40	680	95.5	155	6	ADA95452	Ada95452	Fibroblas
41	680	95.5	155	7	ADC34576	Adc34576	Human fib
42	680	95.5	155	7	ABR56165	Abr56165	Human Fib
43	680	95.5	155	7	ADD66125	Add66125	Fibroblas
44	680	95.5	155	7	ADH92000	Adh92000	Fibroblas
45	680	95.5	155	8	ADO55201	Ado55201	Human aci

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OM protein - protein search, using sw model

Run on: February 16, 2006, 20:46:07 ; Search time 90.4373 Seconds
                                               (without alignments)
                                               609.853 Million cell updates/sec

Title: US-10-049-429-17
Perfect score: 712
Sequence: 1 PGNYKKPKLLYCSNGHFLRI..........PRTHYGQKAILFLPLPVSSD 132

Scoring table: BLOSUM62
                   Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_AA_Main:*
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                   2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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                   4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
                   5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                  SUMMARIES
                      %
Result   Query
  No.   Score   Match Length DB ID   Description
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        3   680   95.5   141   3 US-09-929-945-7   Sequence 7, Appli
        4   680   95.5   141   3 US-09-820-596-7   Sequence 7, Appli
        5   680   95.5   141   4 US-10-280-864-7   Sequence 7, Appli
        6   680   95.5   141   4 US-10-649-480-7   Sequence 7, Appli
        7   680   95.5   154   3 US-09-929-945-8   Sequence 8, Appli
        8   680   95.5   154   4 US-10-280-864-8   Sequence 8, Appli
        9   680   95.5   154   4 US-10-649-480-8   Sequence 8, Appli
       10   680   95.5   155   3 US-09-284-663A-9   Sequence 9, Appli
       11   680   95.5   155   3 US-09-902-773A-3   Sequence 3, Appli

12	680	95.5	155	3	US-09-251-263-9	Sequence 9, Appli
13	680	95.5	155	3	US-09-425-021-9	Sequence 9, Appli
14	680	95.5	155	3	US-09-929-918-2	Sequence 2, Appli
15	680	95.5	155	3	US-09-929-918-11	Sequence 11, Appl
16	680	95.5	155	3	US-09-929-945-2	Sequence 2, Appli
17	680	95.5	155	3	US-09-902-460-4	Sequence 4, Appli
18	680	95.5	155	3	US-09-345-373-16	Sequence 16, Appl
19	680	95.5	155	4	US-10-081-347-29	Sequence 29, Appl
20	680	95.5	155	4	US-10-280-864-2	Sequence 2, Appli
21	680	95.5	155	4	US-10-075-446-16	Sequence 16, Appl
22	680	95.5	155	4	US-10-189-360-10	Sequence 10, Appl
23	680	95.5	155	4	US-10-123-481-3	Sequence 3, Appli
24	680	95.5	155	4	US-10-035-212-16	Sequence 16, Appl
25	680	95.5	155	4	US-10-315-431-29	Sequence 29, Appl
26	680	95.5	155	4	US-10-347-177-8	Sequence 8, Appli
27	680	95.5	155	4	US-10-372-653-7	Sequence 7, Appli
28	680	95.5	155	4	US-10-037-922-29	Sequence 29, Appl
29	680	95.5	155	4	US-10-690-019-5	Sequence 5, Appli
30	680	95.5	155	4	US-10-649-480-2	Sequence 2, Appli
31	680	95.5	155	4	US-10-813-805-2	Sequence 2, Appli
32	680	95.5	155	5	US-10-733-311-16	Sequence 16, Appl
33	680	95.5	155	5	US-10-771-238-22	Sequence 22, Appl
34	680	95.5	155	5	US-10-935-226-3	Sequence 3, Appli
35	680	95.5	155	5	US-10-741-600-1527	Sequence 1527, Ap
36	680	95.5	155	5	US-10-741-600-1530	Sequence 1530, Ap
37	680	95.5	155	5	US-10-741-600-1531	Sequence 1531, Ap
38	680	95.5	155	5	US-10-932-284-3	Sequence 3, Appli
39	680	95.5	155	5	US-10-901-210-16	Sequence 16, Appl
40	680	95.5	155	5	US-10-854-485-29	Sequence 29, Appl
41	680	95.5	155	5	US-10-285-405-5	Sequence 5, Appli
42	680	95.5	155	5	US-10-413-537-9	Sequence 9, Appli
43	680	95.5	155	6	US-11-150-187-4	Sequence 4, Appli
44	678	95.2	155	4	US-10-192-988-13	Sequence 13, Appl
45	674	94.7	139	3	US-09-832-355A-45	Sequence 45, Appl

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 17, 2006, 07:50:38 ; Search time 3475.1 Seconds
                                              (without alignments)
                                              2159.170 Million cell updates/sec

Title: US-10-049-429-17
Perfect score: 712
Sequence: 1 PGNYKKPKLLYCSNGHFLRI..........PRTHYGQKAILFLPLPVSSD 132

Scoring table: BLOSUM62
                  Xgapop 10.0 , Xgapext 0.5
                  Ygapop 10.0 , Ygapext 0.5
                  Fgapop 6.0 , Fgapext 7.0
                  Delop   6.0 , Delext   7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
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-USER=US10049429_@CGN_1_1_5142_@runat_16022006_105606_6251 -NCPU=6 -ICPU=3
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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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                  3: gb_env:*
                  4: gb_om:*
                  5: gb_ov:*
                  6: gb_pat:*
                  7: gb_ph:*
                  8: gb_pr:*
                  9: gb_ro:*
                  10: gb_sts:*
                  11: gb_sy:*
                  12: gb_un:*

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        13:   gb_vi:*
        14:   gb_htg:*
        15:   gb_pl:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                   SUMMARIES
                         %
    Result             Query
       No.    Score   Match Length DB   ID                   Description
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  c      4     680     95.5    454    6   A00070             A00070 Artificial
         5     680     95.5    454    6   E02757             E02757 DNA encodin
         6     680     95.5    454    6   E03043             E03043 cDNA encodi
         7     680     95.5    454    6   E03343             E03343 Synthetic c
         8     680     95.5    454    6   E03692             E03692 cDNA encodi
         9     680     95.5    454    6   E04557             E04557 Human aFGF
        10     680     95.5    454    6   AR362520           AR362520 Sequence
        11     680     95.5    465    6   A01474             A01474 Synthetic g
        12     680     95.5    468    6   CQ848834           CQ848834 Sequence
        13     680     95.5    468    6   CQ855983           CQ855983 Sequence
        14     680     95.5    468    6   AR428605           AR428605 Sequence
        15     680     95.5    468    6   AR575648           AR575648 Sequence
        16     680     95.5    468    6   AX481449           AX481449 Sequence
        17     680     95.5    468   11   AY893033            AY893033 Synthetic
        18     680     95.5    481    6   I08499             I08499 Sequence 13
        19     680     95.5    481    6   I09297             I09297 Sequence 10
        20     680     95.5    490    6   AR380845           AR380845 Sequence
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        22     680     95.5    496    6   A00328             A00328 Artificial
  c     23     680     95.5    496    6   A00329             A00329 Artificial
        24     680     95.5    630    6   AR428604           AR428604 Sequence
        25     680     95.5    630    6   AR428607           AR428607 Sequence
        26     680     95.5    630    6   AR575647           AR575647 Sequence
        27     680     95.5    630    6   AR575650           AR575650 Sequence
        28     680     95.5    638    6   I02042             I02042 Sequence 5
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        32     680     95.5    638    8   HUMECGFB           M13361 Human beta-
        33     680     95.5    990    6   AR575652           AR575652 Sequence
        34     680     95.5   1073    8   BC032697           BC032697 Homo sapi
        35     680     95.5   2251    6   CQ726166           CQ726166 Sequence
        36     680     95.5   2259    8   HSHPGF1            X51943 Human mRNA
        37     680     95.5   2297    6   CQ890894           CQ890894 Sequence
        38     680     95.5   2357    6   CQ875350           CQ875350 Sequence
        39     680     95.5   2357    6   CQ899392           CQ899392 Sequence
        40     680     95.5   2357    6   CQ899442           CQ899442 Sequence
        41     680     95.5   8501    6   A49428             A49428 Sequence 1
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        43     671     94.2    468   11   AY890569            AY890569 Synthetic
        44     667     93.7    405    6   CS131143           CS131143 Sequence
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45   667   93.7   408   6   E37983   E37983 Process for

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 17, 2006, 08:09:24 ; Search time 125.073 Seconds
                                              (without alignments)
                                              1876.011 Million cell updates/sec

Title: US-10-049-429-17
Perfect score: 712
Sequence: 1 PGNYKKPKLLYCSNGHFLRI..........PRTHYGQKAILFLPLPVSSD 132

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss07 -USER=US10049429_@CGN_1_1_237_@runat_16022006_105609_6342 -NCPU=6
-ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Issued_Patents_NA:*
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                 6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                 7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
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                 9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	680	95.5	468	3	US-09-929-945-3	Sequence 3, Appli
3	680	95.5	468	3	US-09-929-918-3	Sequence 3, Appli
4	680	95.5	490	3	US-09-023-655-1390	Sequence 1390, Ap
5	680	95.5	630	3	US-09-929-945-1	Sequence 1, Appli
6	680	95.5	630	3	US-09-929-945-6	Sequence 6, Appli
7	680	95.5	630	3	US-09-929-918-1	Sequence 1, Appli
8	680	95.5	630	3	US-09-929-918-6	Sequence 6, Appli
9	680	95.5	638	3	US-09-098-628-3	Sequence 3, Appli
10	680	95.5	990	3	US-09-929-918-10	Sequence 10, Appl
11	680	95.5	8501	3	US-08-793-900-1	Sequence 1, Appli
12	667	93.7	630	3	US-09-929-945-4	Sequence 4, Appli
13	667	93.7	630	3	US-09-929-918-4	Sequence 4, Appli
14	571.5	80.3	454	3	US-09-030-613-14	Sequence 14, Appl
15	571.5	80.3	454	3	US-09-451-905-14	Sequence 14, Appl
16	555	77.9	450	9	5437995-1	Patent No. 5437995
17	365	51.3	477	2	US-08-290-373B-16	Sequence 16, Appl
18	340	47.8	442	3	US-09-385-114-1	Sequence 1, Appli
19	340	47.8	442	3	US-09-417-721-4	Sequence 4, Appli
20	340	47.8	474	9	5514566-5	Patent No. 5514566
21	338	47.5	1374	3	US-09-366-009-26	Sequence 26, Appl
22	338	47.5	1374	3	US-08-809-156B-26	Sequence 26, Appl
23	338	47.5	1374	3	US-09-775-964-26	Sequence 26, Appl
24	337	47.3	432	3	US-10-168-050-6	Sequence 6, Appli
25	337	47.3	444	9	5175147-9	Patent No. 5175147
26	337	47.3	465	2	US-08-023-757-3	Sequence 3, Appli
27	337	47.3	465	2	US-07-783-694-2	Sequence 2, Appli
28	337	47.3	465	2	US-08-177-502-3	Sequence 3, Appli
29	337	47.3	528	2	US-08-835-231-7	Sequence 7, Appli
30	337	47.3	528	2	US-08-835-231-8	Sequence 8, Appli
31	337	47.3	528	3	US-09-105-678A-1	Sequence 1, Appli
32	337	47.3	528	3	US-09-105-678A-2	Sequence 2, Appli
33	337	47.3	528	3	US-09-105-678A-3	Sequence 3, Appli
34	337	47.3	528	3	US-09-105-678A-4	Sequence 4, Appli
35	337	47.3	528	3	US-09-105-678A-5	Sequence 5, Appli
36	337	47.3	528	3	US-09-105-678A-6	Sequence 6, Appli
37	337	47.3	528	3	US-09-421-208-1	Sequence 1, Appli
38	337	47.3	528	3	US-09-421-208-2	Sequence 2, Appli
39	337	47.3	528	3	US-09-421-208-3	Sequence 3, Appli
40	337	47.3	528	3	US-09-421-208-4	Sequence 4, Appli
41	337	47.3	528	3	US-09-421-208-5	Sequence 5, Appli
42	337	47.3	528	3	US-09-421-208-6	Sequence 6, Appli
43	337	47.3	528	3	US-09-108-661-7	Sequence 7, Appli
44	337	47.3	528	3	US-09-108-661-8	Sequence 8, Appli
45	337	47.3	537	2	US-08-835-231-5	Sequence 5, Appli

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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 17, 2006, 12:45:19 ; Search time 277.854 Seconds
                                              (without alignments)
                                              1008.448 Million cell updates/sec

Title: US-10-049-429-17
Perfect score: 712
Sequence: 1 PGNYKKPKLLYCSNGHFLRI.........PRTHYGQKAILFLPLPVSSD 132

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 7204252 seqs, 1061369211 residues

Total number of hits satisfying chosen parameters: 14408504

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10049429/runat_16022006_105622_6651/app_query.fasta_1
-DB=Published_Applications_NA_New -QFMT=fastap -SUFFIX=rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss02h
-USER=US10049429_@CGN_1_1_380_@runat_16022006_105622_6651 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Published_Applications_NA_New:*
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                 2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
                 3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                 4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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                 10: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
                 11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	620	87.1	1216	12	US-11-136-527-2147	Sequence 2147, Ap
2	340	47.8	442	12	US-11-220-027-1	Sequence 1, Appli
3	340	47.8	442	12	US-11-238-936-4	Sequence 4, Appli
4	338	47.5	1374	9	US-11-181-091-26	Sequence 26, Appl
5	334	46.9	1991	12	US-11-136-527-3242	Sequence 3242, Ap
6	331	46.5	489	12	US-11-220-027-4	Sequence 4, Appli
7	331	46.5	6774	8	US-10-995-561-436	Sequence 436, App
8	331	46.5	6802	12	US-11-169-041-26	Sequence 26, Appl
9	308	43.3	1786	12	US-11-136-527-2517	Sequence 2517, Ap
c 10	240	33.7	600	12	US-11-136-527-7338	Sequence 7338, Ap
11	239.5	33.6	537	8	US-10-980-459-41	Sequence 41, Appl
12	239.5	33.6	540	8	US-10-842-206-23	Sequence 23, Appl
13	239.5	33.6	540	8	US-10-980-459-9	Sequence 9, Appli
14	239.5	33.6	549	8	US-10-842-206-13	Sequence 13, Appl
15	239.5	33.6	556	8	US-10-842-206-7	Sequence 7, Appli
16	239.5	33.6	633	8	US-10-842-206-3	Sequence 3, Appli
17	239.5	33.6	633	8	US-10-842-206-35	Sequence 35, Appl
18	239.5	33.6	633	8	US-10-980-459-1	Sequence 1, Appli
19	239.5	33.6	633	8	US-10-980-459-21	Sequence 21, Appl
20	239.5	33.6	636	8	US-10-842-206-21	Sequence 21, Appl
21	239.5	33.6	636	8	US-10-980-459-5	Sequence 5, Appli
22	238.5	33.5	447	8	US-10-980-459-35	Sequence 35, Appl
23	238.5	33.5	466	8	US-10-842-206-11	Sequence 11, Appl
24	238.5	33.5	477	8	US-10-842-206-19	Sequence 19, Appl
25	238.5	33.5	477	8	US-10-980-459-3	Sequence 3, Appli
26	238.5	33.5	567	8	US-10-980-459-31	Sequence 31, Appl
27	238.5	33.5	594	8	US-10-980-459-29	Sequence 29, Appl
28	238.5	33.5	600	12	US-11-136-527-6842	Sequence 6842, Ap
29	238.5	33.5	603	8	US-10-980-459-27	Sequence 27, Appl
30	238.5	33.5	612	8	US-10-980-459-25	Sequence 25, Appl
31	238.5	33.5	630	8	US-10-980-459-23	Sequence 23, Appl
32	238.5	33.5	636	8	US-10-842-206-1	Sequence 1, Appli
33	238.5	33.5	636	8	US-10-980-459-8	Sequence 8, Appli
34	238.5	33.5	639	12	US-11-136-527-2746	Sequence 2746, Ap
35	237.5	33.4	402	8	US-10-980-459-33	Sequence 33, Appl
36	237.5	33.4	415	8	US-10-842-206-9	Sequence 9, Appli
37	235.5	33.1	540	8	US-10-842-206-5	Sequence 5, Appli
38	235.5	33.1	540	8	US-10-980-459-6	Sequence 6, Appli
39	234.5	32.9	408	8	US-10-842-206-17	Sequence 17, Appl
40	234.5	32.9	1084	12	US-11-136-527-1812	Sequence 1812, Ap
41	233.5	32.8	396	8	US-10-980-459-39	Sequence 39, Appl
42	233.5	32.8	408	8	US-10-842-206-15	Sequence 15, Appl
43	232.5	32.7	396	8	US-10-980-459-37	Sequence 37, Appl
44	226.5	31.8	624	12	US-11-136-527-2611	Sequence 2611, Ap
45	226.5	31.8	624	12	US-11-136-527-6707	Sequence 6707, Ap

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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 17, 2006, 07:55:47 ; Search time 2792.4 Seconds
                                              (without alignments)
                                              2211.683 Million cell updates/sec

Title: US-10-049-429-17
Perfect score: 712
Sequence: 1 PGNYKKPKLLYCSNGHFLRI..........PRTHYGQKAILFLPLPVSSD 132

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02h
-USER=US10049429_@CGN_1_1_6731_@runat_16022006_105607_6293 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   EST:*
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                 4: gb_htc:*
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                 7: gb_est6:*
                 8: gb_est7:*
                 9: gb_gss1:*
                 10: gb_gss2:*
                 11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	680	95.5	534	1	AI590078	AI590078 tm58c01.x
2	680	95.5	625	7	CV030767	CV030767 9975 Full
3	680	95.5	821	3	BI598390	BI598390 603250094
4	680	95.5	1014	3	BM809005	BM809005 AGENCOURT
5	680	95.5	1098	5	BX444567	BX444567 BX444567
6	680	95.5	2614	4	CR925957	CR925957 Pongo pyg
7	667	93.7	1057	3	BQ067949	BQ067949 AGENCOURT
8	656	92.1	508	10	CG633840	CG633840 OST353987
9	656	92.1	628	8	CX733346	CX733346 oc42c07.y
10	656	92.1	635	7	CK624469	CK624469 mi21e12.y
11	656	92.1	787	8	CX244360	CX244360 NMA02246
12	656	92.1	855	3	BI331990	BI331990 602984393
13	656	92.1	3404	4	AK035330	AK035330 Mus muscu
14	650	91.3	663	1	AI119291	AI119291 ue95c07.y
15	650	91.3	714	2	BG706412	BG706412 602669744
16	650	91.3	878	3	BI753845	BI753845 603027526
17	640	89.9	832	3	BI869731	BI869731 603393620
c 18	633	88.9	472	1	AI077609	AI077609 oy26d02.s
19	629	88.3	596	8	DN375385	DN375385 LIB38529_
20	623.5	87.6	843	3	BI692283	BI692283 603342751
21	623.5	87.6	2206	4	BC027001	BC027001 Mus muscu
22	613	86.1	631	2	BB627624	BB627624 BB627624
23	612	86.0	461	2	BF956865	BF956865 RC1-NN023
24	610	85.7	809	7	CO420661	CO420661 GGEZHC101
25	591	83.0	689	1	AI663400	AI663400 uk32d07.y
26	575	80.8	813	2	BF532970	BF532970 602073491
27	564.5	79.3	611	5	BU840197	BU840197 AGENCOURT
28	563	79.1	584	8	DN993277	DN993277 TC111631
29	541	76.0	526	10	CG565930	CG565930 OST191133
30	526.5	73.9	503	2	BF442355	BF442355 259038 MA
c 31	507.5	71.3	750	5	BU627243	BU627243 UI-H-FG0-
32	484	68.0	926	6	CD253719	CD253719 AGENCOURT
33	481.5	67.6	529	10	CG629018	CG629018 OST340697
34	478.5	67.2	638	7	CN315070	CN315070 170005326
35	478.5	67.2	697	6	CD634782	CD634782 56070641H
c 36	475.5	66.8	429	1	AW531286	AW531286 UI-R-C4-a
37	472	66.3	546	7	CR533323	CR533323 DKFZp459M
c 38	468.5	65.8	364	1	AI864448	AI864448 wl53c07.x
39	468.5	65.8	570	3	BI598882	BI598882 603247981
c 40	466.5	65.5	415	1	AI083919	AI083919 qf26c07.x
41	463.5	65.1	288	6	CB710781	CB710781 AMGNNUC:N
42	462	64.9	543	1	AA261582	AA261582 mz87c09.r
c 43	439.5	61.7	701	3	BM995210	BM995210 UI-H-ED0-
44	438	61.5	469	1	AW259195	AW259195 um89f09.y
45	435	61.1	395	6	CB773841	CB773841 AMGNNUC:S

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OM protein - protein search, using sw model

Run on:           February 16, 2006, 20:30:32 ; Search time 26.1691 Seconds
                                              (without alignments)
                                              417.026 Million cell updates/sec


Title:            US-10-049-429-17
Perfect score:    712
Sequence:         1 PGNYKKPKLLYCSNGHFLRI..........PRTHYGQKAILFLPLPVSSD 132


Scoring table:    BLOSUM62
                  Gapop 10.0 , Gapext 0.5  .


Searched:         572060 seqs, 82675679 residues


Total number of hits satisfying chosen parameters:       572060


Minimum DB seq length: 0
Maximum DB seq length: 2000000000


Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries


Database :        Issued_Patents_AA:*
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                  3:  /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
                  4:  /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                  5:  /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                  6:  /cgn2_6/ptodata/1/iaa/backfiles1.pep:*


       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.


                                  SUMMARIES
                       %
Result                 Query
    No.    Score    Match Length DB  ID                          Description
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       2     680     95.5     140  6  5464943-28                  Patent No. 5464943
       3     680     95.5     141  2  US-09-929-945-7             Sequence 7, Appli
       4     680     95.5     141  2  US-09-929-918-7             Sequence 7, Appli
       5     680     95.5     154  2  US-09-929-945-8             Sequence 8, Appli
       6     680     95.5     155  1  US-08-439-725A-9            Sequence 9, Appli
       7     680     95.5     155  1  US-08-464-590A-13           Sequence 13, Appl
       8     680     95.5     155  1  US-08-462-169B-9            Sequence 9, Appli
       9     680     95.5     155  1  US-08-207-412B-8            Sequence 8, Appli
      10     680     95.5     155  1  US-08-867-471-9             Sequence 9, Appli
      11     680     95.5     155  1  US-08-951-822-29            Sequence 29, Appl
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12	680	95.5	155	2	US-09-103-079-9	Sequence 9, Appli
13	680	95.5	155	2	US-08-705-245-5	Sequence 5, Appli
14	680	95.5	155	2	US-08-718-904-10	Sequence 10, Appl
15	680	95.5	155	2	US-09-023-082A-16	Sequence 16, Appl
16	680	95.5	155	2	US-09-093-585-13	Sequence 13, Appl
17	680	95.5	155	2	US-09-098-628-4	Sequence 4, Appli
18	680	95.5	155	2	US-09-368-951-29	Sequence 29, Appl
19	680	95.5	155	2	US-09-425-021-9	Sequence 9, Appli
20	680	95.5	155	2	US-09-449-249-10	Sequence 10, Appl
21	680	95.5	155	2	US-09-390-207-14	Sequence 14, Appl
22	680	95.5	155	2	US-09-229-947-29	Sequence 29, Appl
23	680	95.5	155	2	US-09-564-829-3	Sequence 3, Appli
24	680	95.5	155	2	US-09-248-998-16	Sequence 16, Appl
25	680	95.5	155	2	US-09-572-406B-7	Sequence 7, Appli
26	680	95.5	155	2	US-09-490-714-5	Sequence 5, Appli
27	680	95.5	155	2	US-09-929-945-2	Sequence 2, Appli
28	680	95.5	155	2	US-09-610-651-16	Sequence 16, Appl
29	680	95.5	155	2	US-09-929-918-2	Sequence 2, Appli
30	680	95.5	155	2	US-09-929-918-11	Sequence 11, Appl
31	680	95.5	155	2	US-09-345-373-16	Sequence 16, Appl
32	680	95.5	155	2	US-10-075-446-16	Sequence 16, Appl
33	678	95.2	155	1	US-08-438-439C-13	Sequence 13, Appl
34	673	94.5	136	6	5437995-2	Patent No. 5437995
35	669.5	94.0	156	2	US-09-030-613-15	Sequence 15, Appl
36	669.5	94.0	156	2	US-09-451-905-15	Sequence 15, Appl
37	667	93.7	135	2	US-09-929-945-5	Sequence 5, Appli
38	667	93.7	135	2	US-09-929-918-5	Sequence 5, Appli
39	657.5	92.3	191	1	US-08-438-439C-22	Sequence 22, Appl
40	656	92.1	155	2	US-09-390-207-24	Sequence 24, Appl
41	655	92.0	140	2	US-09-417-721-1	Sequence 1, Appli
42	655	92.0	140	2	US-09-377-675A-8	Sequence 8, Appli
43	626	87.9	140	1	US-07-830-330-7	Sequence 7, Appli
44	626	87.9	140	1	US-08-187-780-4	Sequence 4, Appli
45	626	87.9	140	1	US-08-478-485-4	Sequence 4, Appli

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OM protein - protein search, using sw model

Run on: February 16, 2006, 20:46:52 ; Search time 8.46647 Seconds
                                              (without alignments)
                                              221.619 Million cell updates/sec

Title: US-10-049-429-17
Perfect score: 712
Sequence: 1 PGNYKKPKLLYCSNGHFLRI.........PRTHYGQKAILFLPLPVSSD 132

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 107819 seqs, 14214640 residues

Total number of hits satisfying chosen parameters: 107819

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_AA_New:*
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                 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
                 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
                 4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
                 5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
                 6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
                 7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
                 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES
                   %
Result   Query
   No.   Score   Match Length DB   ID   Description
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     1   680   95.5   155   7   US-11-149-462-7   Sequence 7, Appli
     2   655   92.0   140   7   US-11-238-936-1   Sequence 1, Appli
     3   598   84.0   140   7   US-11-238-936-2   Sequence 2, Appli
     4   340   47.8   146   7   US-11-220-027-2   Sequence 2, Appli
     5   340   47.8   146   7   US-11-238-936-5   Sequence 5, Appli
     6   338   47.5   457   7   US-11-181-091-5   Sequence 5, Appli
     7   331   46.5   146   7   US-11-220-027-6   Sequence 6, Appli
     8   331   46.5   146   7   US-11-238-936-3   Sequence 3, Appli
     9   331   46.5   155   6   US-10-995-561-953   Sequence 953, App

10	331	46.5	155	7	US-11-220-027-5	Sequence 5, Appli
11	331	46.5	155	7	US-11-181-091-3	Sequence 3, Appli
12	331	46.5	196	7	US-11-169-041-154	Sequence 154, App
13	331	46.5	288	7	US-11-149-462-8	Sequence 8, Appli
14	331	46.5	432	7	US-11-181-091-4	Sequence 4, Appli
15	316.5	44.5	145	7	US-11-021-305-5	Sequence 5, Appli
16	238.5	33.5	149	6	US-10-980-459-36	Sequence 36, Appl
17	238.5	33.5	155	6	US-10-842-206-12	Sequence 12, Appl
18	238.5	33.5	158	6	US-10-842-206-20	Sequence 20, Appl
19	238.5	33.5	158	6	US-10-980-459-4	Sequence 4, Appli
20	238.5	33.5	179	6	US-10-842-206-24	Sequence 24, Appl
21	238.5	33.5	179	6	US-10-980-459-10	Sequence 10, Appl
22	238.5	33.5	183	6	US-10-842-206-14	Sequence 14, Appl
23	238.5	33.5	185	6	US-10-842-206-8	Sequence 8, Appli
24	238.5	33.5	188	6	US-10-842-206-40	Sequence 40, Appl
25	238.5	33.5	188	6	US-10-980-459-32	Sequence 32, Appl
26	238.5	33.5	197	6	US-10-842-206-39	Sequence 39, Appl
27	238.5	33.5	197	6	US-10-980-459-30	Sequence 30, Appl
28	238.5	33.5	200	6	US-10-842-206-38	Sequence 38, Appl
29	238.5	33.5	200	6	US-10-980-459-28	Sequence 28, Appl
30	238.5	33.5	203	6	US-10-842-206-37	Sequence 37, Appl
31	238.5	33.5	203	6	US-10-980-459-26	Sequence 26, Appl
32	238.5	33.5	209	6	US-10-980-459-24	Sequence 24, Appl
33	238.5	33.5	211	6	US-10-842-206-2	Sequence 2, Appli
34	238.5	33.5	211	6	US-10-842-206-4	Sequence 4, Appli
35	238.5	33.5	211	6	US-10-842-206-22	Sequence 22, Appl
36	238.5	33.5	211	6	US-10-842-206-36	Sequence 36, Appl
37	238.5	33.5	211	6	US-10-980-459-2	Sequence 2, Appli
38	238.5	33.5	211	6	US-10-980-459-22	Sequence 22, Appl
39	237.5	33.4	134	6	US-10-980-459-34	Sequence 34, Appl
40	237.5	33.4	138	6	US-10-842-206-10	Sequence 10, Appl
41	234.5	32.9	136	6	US-10-842-206-18	Sequence 18, Appl
42	234.5	32.9	179	6	US-10-842-206-6	Sequence 6, Appli
43	234.5	32.9	179	6	US-10-980-459-7	Sequence 7, Appli
44	234.5	32.9	208	7	US-11-238-936-13	Sequence 13, Appl
45	233.5	32.8	132	6	US-10-980-459-40	Sequence 40, Appl

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 17, 2006, 07:21:59 ; Search time 412.163 Seconds
                                              (without alignments)
                                              2134.444 Million cell updates/sec

Title: US-10-049-429-17
Perfect score: 712
Sequence: 1 PGNYKKPKLLYCSNGHFLRI..........PRTHYGQKAILFLPLPVSSD 132

Scoring table: BLOSUM62
                  Xgapop 10.0 , Xgapext 0.5
                  Ygapop 10.0 , Ygapext 0.5
                  Fgapop 6.0 , Fgapext 7.0
                  Delop   6.0 , Delext   7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10049429/runat_16022006_105604_6239/app_query.fasta_1
-DB=N_Geneseq -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss07
-USER=US10049429_@CGN_1_1_900_@runat_16022006_105604_6239 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   N_Geneseq_21:*
                  1: geneseqn1980s:*
                  2: geneseqn1990s:*
                  3: geneseqn2000s:*
                  4: geneseqn2001as:*
                  5: geneseqn2001bs:*
                  6: geneseqn2002as:*
                  7: geneseqn2002bs:*
                  8: geneseqn2003as:*
                  9: geneseqn2003bs:*
                  10: geneseqn2003cs:*
                  11: geneseqn2003ds:*
                  12: geneseqn2004as:*

13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	680	95.5	440	1	AAN90117	Aan90117 Human aci
2	680	95.5	454	2	AAQ02421	Aaq02421 cDNA enco
3	680	95.5	454	2	AAQ03873	Aaq03873 Synthetic
4	680	95.5	454	2	AAQ10399	Aaq10399 Human aci
5	680	95.5	454	2	AAQ10166	Aaq10166 Human aci
6	680	95.5	454	2	AAQ25916	Aaq25916 aFGF mute
7	680	95.5	462	2	AAT45983	Aat45983 Human end
8	680	95.5	465	1	AAN92890	Aan92890 Synthetic
9	680	95.5	465	10	ADL13663	Adl13663 Osteoarth
10	680	95.5	468	6	ABV78179	Abv78179 Human DNA
11	680	95.5	468	6	ABZ35755	Abz35755 Human pol
12	680	95.5	468	6	ABX09998	Abx09998 Human DNA
13	680	95.5	468	6	AAK98918	Aak98918 Human aci
14	680	95.5	468	6	ABL91720	Abl91720 Human pol
15	680	95.5	468	10	ADL13661	Adl13661 Osteoarth
16	680	95.5	468	12	ADO55202	Ado55202 Human aci
17	680	95.5	468	13	ADQ94629	Adq94629 Human FGF
18	680	95.5	468	14	ADV42741	Adv42741 Human psy
19	680	95.5	481	1	AAN71029	Aan71029 Sequence
20	680	95.5	481	1	AAN90994	Aan90994 Partially
21	680	95.5	490	11	ADI32064	Adi32064 Human cDN
22	680	95.5	490	13	ADS84131	Ads84131 Human lym
23	680	95.5	496	2	AAQ03871	Aaq03871 Synthetic
c 24	680	95.5	527	14	ACL55684	Acl55684 Human col
25	680	95.5	630	6	ABK10592	Abk10592 cDNA enco
26	680	95.5	630	6	ABK10595	Abk10595 cDNA enco
27	680	95.5	630	6	AAK98917	Aak98917 Codon opt
28	680	95.5	630	6	AAK98920	Aak98920 Codon opt
29	680	95.5	630	12	ADO55200	Ado55200 Human aci
30	680	95.5	630	12	ADO55205	Ado55205 Human aci
31	680	95.5	638	1	AAN70788	Aan70788 Complete
32	680	95.5	638	1	AAN93088	Aan93088 Acidic fi
33	680	95.5	638	2	AAT37503	Aat37503 Human bet
34	680	95.5	638	2	AAV34350	Aav34350 Human end
35	680	95.5	638	2	AAX01723	Aax01723 Human end
36	680	95.5	638	9	ACF04028	Acf04028 Thrombin
37	680	95.5	639	2	AAT45985	Aat45985 Human end
38	680	95.5	920	10	ADL13664	Adl13664 Osteoarth
39	680	95.5	990	6	AAK98922	Aak98922 Codon opt
40	680	95.5	2259	10	ADL13660	Adl13660 Osteoarth
41	680	95.5	2297	13	ADT89313	Adt89313 Human aci
42	680	95.5	2357	10	ACC42968	Acc42968 Human Fib
43	680	95.5	2357	13	ADR67193	Adr67193 Human bla
44	680	95.5	2357	13	ADU18122	Adu18122 Human can
45	680	95.5	2357	13	ADU18061	Adu18061 Human can

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 17, 2006, 12:27:39 ; Search time 551.86 Seconds
                                                (without alignments)
                                                1977.961 Million cell updates/sec

Title: US-10-049-429-17
Perfect score: 712
Sequence: 1 PGNYKKPKLLYCSNGHFLRI..........PRTHYGQKAILFLPLPVSSD 132

Scoring table: BLOSUM62
                  Xgapop 10.0 , Xgapext 0.5
                  Ygapop 10.0 , Ygapext 0.5
                  Fgapop 6.0 , Fgapext 7.0
                  Delop   6.0 , Delext   7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10049429/runat_16022006_105619_6597/app_query.fasta_1
-DB=Published_Applications_NA_Main -QFMT=fastap -SUFFIX=rnpbm -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss02h
-USER=US10049429_@CGN_1_1_1364_@runat_16022006_105619_6597 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Published_Applications_NA_Main:*
                  1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
                  2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
                  3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
                  4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
                  5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
                  6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
                  7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
                  8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
                  9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
                  10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	680	95.5	468	3	US-09-929-918-3	Sequence 3, Appli
2	680	95.5	468	3	US-09-929-945-3	Sequence 3, Appli
3	680	95.5	468	5	US-10-280-864-3	Sequence 3, Appli
4	680	95.5	468	7	US-10-649-480-3	Sequence 3, Appli
5	680	95.5	468	7	US-10-384-339C-63	Sequence 63, Appl
6	680	95.5	490	6	US-10-388-410-8	Sequence 8, Appli
7	680	95.5	490	7	US-10-641-643-1390	Sequence 1390, Ap
8	680	95.5	630	3	US-09-929-918-1	Sequence 1, Appli
9	680	95.5	630	3	US-09-929-918-6	Sequence 6, Appli
10	680	95.5	630	3	US-09-929-945-1	Sequence 1, Appli
11	680	95.5	630	3	US-09-929-945-6	Sequence 6, Appli
12	680	95.5	630	5	US-10-280-864-1	Sequence 1, Appli
13	680	95.5	630	5	US-10-280-864-6	Sequence 6, Appli
14	680	95.5	630	7	US-10-649-480-1	Sequence 1, Appli
15	680	95.5	630	7	US-10-649-480-6	Sequence 6, Appli
16	680	95.5	638	3	US-09-902-460-3	Sequence 3, Appli
17	680	95.5	638	10	US-11-150-187-3	Sequence 3, Appli
18	680	95.5	990	3	US-09-929-918-10	Sequence 10, Appl
19	680	95.5	2297	8	US-10-813-805-1	Sequence 1, Appli
20	680	95.5	2357	9	US-10-956-157-461	Sequence 461, App
21	680	95.5	2357	9	US-10-285-405-6	Sequence 6, Appli
22	680	95.5	3289	8	US-10-741-600-702	Sequence 702, App
23	680	95.5	3677	8	US-10-741-600-699	Sequence 699, App
24	680	95.5	4083	8	US-10-741-600-703	Sequence 703, App
25	680	95.5	4087	5	US-10-044-090-225	Sequence 225, App
26	667	93.7	630	3	US-09-929-918-4	Sequence 4, Appli
27	667	93.7	630	3	US-09-929-945-4	Sequence 4, Appli
28	667	93.7	630	5	US-10-280-864-4	Sequence 4, Appli
29	667	93.7	630	7	US-10-649-480-4	Sequence 4, Appli
30	656	92.1	468	8	US-10-813-805-3	Sequence 3, Appli
31	478.5	67.2	3225	8	US-10-741-600-701	Sequence 701, App
32	478.5	67.2	3979	8	US-10-741-600-704	Sequence 704, App
33	474	66.6	3821	8	US-10-741-600-700	Sequence 700, App
34	353	49.6	3658	3	US-09-968-007A-133	Sequence 133, App
35	353	49.6	3658	3	US-09-968-007A-440	Sequence 440, App
36	353	49.6	3658	8	US-10-788-792-48	Sequence 48, Appl
37	353	49.6	3658	9	US-10-843-641A-6603	Sequence 6603, Ap
38	353	49.6	3658	9	US-10-843-641A-6910	Sequence 6910, Ap
39	353	49.6	106236	8	US-10-741-600-17759	Sequence 17759, A
40	340	47.8	441	3	US-09-802-365-1	Sequence 1, Appli
41	340	47.8	441	3	US-09-886-856-1	Sequence 1, Appli
42	340	47.8	441	8	US-10-845-911-1	Sequence 1, Appli
43	340	47.8	442	3	US-09-771-302-1	Sequence 1, Appli
44	340	47.8	442	5	US-10-131-965-4	Sequence 4, Appli
45	340	47.8	442	6	US-10-184-708-1	Sequence 1, Appli

OM protein - protein search, using sw model

Run on: February 16, 2006, 20:25:36 ; Search time 18.8571 Seconds
                                              (without alignments)
                                 673.517 Million cell updates/sec

Title: US-10-049-429-17
Perfect score: 712
Sequence: 1 PGNYKKPKLLYCSNGHFLRI.........PRTHYGQKAILFLPLPVSSD 132

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_80:*
                 1: pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	680	95.5	155	1	A33665	acidic fibroblast
2	667	93.7	155	1	A60721	acidic fibroblast
3	656	92.1	155	2	D37360	acidic fibroblast
4	656	92.1	155	2	S04147	acidic fibroblast
5	650	91.3	152	2	JH0476	acidic fibroblast
6	626	87.9	155	1	GKBOA	acidic fibroblast
7	618	86.8	155	2	JW0055	acidic fiblobrast
8	610	85.7	155	2	A60130	acidic fibroblast
9	340	47.8	146	1	S00185	basic fibroblast g
10	340	47.8	157	1	GKBOB	basic fibroblast g
11	339	47.6	189	2	A48834	basic fibroblast g
12	334	46.9	154	2	C37360	basic fibroblast g
13	334	46.9	154	2	A31674	basic fibroblast g

14	331	46.5	210	2	A32398	basic fibroblast g
15	326	45.8	164	2	S31622	basic fibroblast g
16	319	44.8	155	1	A40117	basic fibroblast g
17	306	43.0	137	2	I46711	fibroblast growth
18	238.5	33.5	211	2	JC7353	fibroblast growth
19	237.5	33.4	212	2	JC7511	fibroblast growth
20	234.5	32.9	208	2	S66486	fibroblast growth
21	234.5	32.9	208	2	A48137	fibroblast growth
22	231.5	32.5	208	2	JC7082	fibroblast somatot
23	230.5	32.4	207	2	JC5941	fibroblast growth
24	226.5	31.8	207	2	JC5940	fibroblast growth
25	219.5	30.8	256	2	JC4627	fibroblast growth
26	208.5	29.3	220	2	I50588	fibroblast growth
27	205.5	28.9	237	1	S39582	transforming prote
28	202	28.4	245	1	TVMST2	transforming prote
29	197	27.7	239	1	S04742	fibroblast growth
30	196	27.5	187	2	S23595	embryonic fibrobla
31	188.5	26.5	194	2	S49501	keratinocyte growt
32	188	26.4	194	2	I50710	fibroblast growth
33	186.5	26.2	194	2	I48610	keratinocyte growt
34	185.5	26.1	168	2	JG0184	fibroblast growth
35	185.5	26.1	194	2	S26049	fibroblast growth
36	184.5	25.9	194	1	A36301	fibroblast growth
37	184	25.8	192	2	S54407	embryonic fibrobla
38	182.5	25.6	125	2	A32484	basic fibroblast g
39	180.5	25.4	413	2	H88481	protein let-756 [i
40	174	24.4	206	2	JC4268	fibroblast growth
41	173	24.3	264	2	A36207	fibroblast growth
42	173	24.3	266	2	S68144	fibroblast growth
43	173	24.3	267	1	TVHUF5	fibroblast growth
44	172	24.2	206	1	TVHUHS	fibroblast growth
45	171.5	24.1	60	2	JH0708	fibroblast growth

OM protein - protein search, using sw model

Run on: February 16, 2006, 20:21:06 ; Search time 113.528 Seconds
                                              (without alignments)
                                  820.326 Million cell updates/sec

Title: US-10-049-429-17
Perfect score: 712
Sequence: 1 PGNYKKPKLLYCSNGHFLRI.........PRTHYGQKAILFLPLPVSSD 132

Scoring table: BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   UniProt_05.80:*
                  1: uniprot_sprot:*
                  2: uniprot_trembl:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                SUMMARIES
                        %
Result   Query
   No.   Score   Match Length DB   ID   Description
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     1   680   95.5   155   1   FGF1_HUMAN   P05230 homo sapien
     2   680   95.5   214   2   Q5NVQ3_PONPY   Q5nvq3 pongo pygma
     3   667   93.7   155   1   FGF1_MESAU   P34004 mesocricetu
     4   656   92.1   155   1   FGF1_MOUSE   P61148 mus musculu
     5   656   92.1   155   1   FGF1_RAT   P61149 rattus norv
     6   656   92.1   155   2   Q6ZWS1_MOUSE   Q6zws1 mus musculu
     7   650   91.3   152   1   FGF1_PIG   P20002 sus scrofa
     8   646   90.7   131   2   Q5ISN2_MACFA   Q5isn2 macaca fasc
     9   626   87.9   155   1   FGF1_BOVIN   P03968 b heparin-b
    10   618   86.8   155   1   FGF1_SHEEP   Q7m303 ovis aries
    11   610   85.7   155   1   FGF1_CHICK   P19596 gallus gall
    12   537   75.4   148   1   FGF1_CYNPY   Q6i6m7 cynops pyrr
    13   517   72.6   132   1   FGF1_NOTVI   Q7sif8 notophthalm
    14   510   71.6   155   1   FGF1_XENLA   Q6glr6 xenopus lae
    15   478   67.1   106   1   FGF1_CAPCA   Q9nls8 capreolus c

16	385	54.1	141	2	Q4SJV9_TETNG	Q4sjv9 tetraodon n
17	353	49.6	64	2	Q6LBM3_HUMAN	Q6lbm3 homo sapien
18	348	48.9	64	2	Q71UP6_MOUSE	Q71up6 mus musculu
19	340	47.8	155	1	FGF2_BOVIN	P03969 bos taurus
20	340	47.8	155	1	FGF2_SHEEP	P20003 ovis aries
21	340	47.8	155	2	Q4JH23_SHEEP	Q4jh23 ovis aries
22	339	47.6	147	2	Q5TLE3_BRARE	Q5tle3 brachydanio
23	339	47.6	154	2	Q7ZZK5_BRARE	Q7zzk5 brachydanio
24	339	47.6	155	2	Q5FXK5_ONCMY	Q5fxk5 oncorhynchu
25	339	47.6	158	1	FGF2_CHICK	P48800 gallus gall
26	335	47.1	188	2	Q4S3V1_TETNG	Q4s3v1 tetraodon n
27	334	46.9	154	1	FGF2_MOUSE	P15655 mus musculu
28	334	46.9	154	1	FGF2_RAT	P13109 rattus norv
29	334	46.9	154	2	Q541T2_MOUSE	Q541t2 mus musculu
30	333	46.8	147	1	FGF1_BRARE	Q6pbt8 brachydanio
31	331	46.5	146	2	Q5PY50_HUMAN	Q5py50 homo sapien
32	331	46.5	155	1	FGF2_HUMAN	P09038 homo sapien
33	331	46.5	196	2	P78443_HUMAN	P78443 homo sapien
34	331	46.5	210	2	Q7KZ72_HUMAN	Q7kz72 homo sapien
35	331	46.5	288	2	Q5IS69_PANTR	Q5is69 pan troglod
36	328	46.1	155	2	Q8QFR9_FUGRU	Q8qfr9 fugu rubrip
37	326	45.8	156	1	FGF2_MONDO	P48798 monodelphis
38	325	45.6	130	2	O77767_CANFA	O77767 canis famil
39	322.5	45.3	153	2	Q925A3_MOUSE	Q925a3 mus musculu
40	319	44.8	155	1	FGF2_XENLA	P12226 xenopus lae
41	318.5	44.7	128	2	Q4RIS1_TETNG	Q4ris1 tetraodon n
42	316	44.4	155	2	Q90Y92_CYNPY	Q90y92 cynops pyrr
43	306	43.0	137	1	FGF2_RABIT	P48799 oryctolagus
44	299	42.0	170	1	FGF2_CAVPO	Q60487 cavia porce
45	279	39.2	125	2	Q98TD8_CYNPY	Q98td8 cynops pyrr